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Database :
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Maximum Match 100%
Listing first 45 summaries
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2: /SIDS2/gcgdata/g
3: /SIDS2/gcgdata/qq
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993_DAT:*
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ALIGNMENTS

RESULT 1

AAW37370 standard; Protein; 162 AA

AAW37370;

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25-APR-1997;
                                             /label= Q149D /note= "wild-type Gln is substituted by Asp" Misc-difference 156..0
              06-NOV-1997.
                           W09741232-A1
                                                                /note= "mature protein" Misc-difference 149
                                                                                           Peptide
                                                                                                             Synthetic.
                                                                                                                   Homo sapiens.
97WO-US06931.
                                                                            /note= "signal sequence"
49..162
                                 /note= "wild-type Gln is substituted by Asp"
                                                                                              Location/Qualifiers
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Interleukin·15; IL-15; mutant; human; treatment; autoimmune disease; psoriasis; multiple sclerosis; rheumatic arthritis; immune response;

Mutant interleukin-15 (IL-15). 07-MAY-1998 (first entry)

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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or a rheumatic disease selected from systemic lupus crythematosus (SLE), Sjogren's syndrome, scleroderma, mixed connective tissue disease, dermatomyositis, polymyositis, Reiter's syndrome and Behcet's disease. It can also be used to treat Hashimoto's thyroiditis, Grave's disease, multiple sclerosis, myastheria gravis, encephalomyelitis, a variety of pemphigus, psoriasis, inflammatory bowel disease, AIDS and vascular injury. The mutant II-15 can also be used for reducing the viability of a cell that expresses a II-15 receptor. It can also be used to diagnose a disease treatable with an II-15 antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases e.g psoriasis, multiple sclerosis etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutant interleukin 15 polypeptide(s) - used for treating auto-immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specifically binds to a cell surface receptor. The mutant IL-15 is used for suppressing the immune response in a patient. It can be used for treating autoimmune diseases such as rheumatic arthritis, type I diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the mutant interleukin-15 (IL-15) polypeptide. The wild-type IL-15 sequence can be mutated at codon positions 149 and 156 to create IL-15 sequence can be mutated at codon positions 149 and 156 to create this mutant IL-15 polypeptide. This mutant polypeptide is at least 90% the wild-type IL-15 and is capable of inhibiting at least one of the cellular events that normally occurs when the wild-type IL-15 one of the cellular events that normally occurs when the wild-type IL-15 is used specifically binds to a cell surface receptor. The mutant IL-15 is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 57; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                              immune response; autoimmune disease; rheumatoid arthritis; psoriasis; Reiter's syndrome; type I diabetes; Graves' disease; multiple scderosis; Inflammatory bowel disease; acquired immune deficiency syndrome; AIDS; transplantation; graft versus host disease; T-cell death; AICD; activation induced cell death; passive cell death; ADCC; CDC; activation induced cell-mediated cytotoxicity; mutant; mutein; antibody dependent cell-mediated cytotoxicity; mutant; mutein;
                                                                                                                                                                                                                  Human; interleukin-15 receptor; IL-15R; interleukin-2 receptor; IL-2R;
                                                                                                                                                                                                                                                               Human IL-15 double mutant (Q149D and Q156D).
                                                                                                                                                                                                                                                                                                                                                     AAU77994;
                                                                                                                                                                                                                                                                                                                                                                                                 AAU77994 standard; Protein; 162 AA
                                                                                                                                                                                                                                                                                                             02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
Synthetic
                                                                complement directed cytotoxicity.
                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVEILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRISKPHLRSISIOCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1997-549734/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 AA;
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                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 835; DB 18; 100.0%; Pred. No. 6.2e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Misc-difference 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200222805-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                      useful in patients having received a transplant organ, tissue or cell, and in patients having graft versus host disease. The pharmaceutical compositions are useful for promoting T-cell death which includes AICD (activation induced cell death), passive cell death, ADCC (antibody dependent cell-mediated cytotoxicity) or CDC (complement directed dependent cell-mediated cytotoxicity). The present sequence representing human IL-15 double cytotoxicity). The present sequence representing human includes the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapeutic composition is useful for suppressing an immune response in a patient where the patient has or is at risk of developing an immune disease, particularly an autoimmune disease such a rheumatoid arthritis, disease, particularly an autoimmune disease such a rheumatoid arthritis, Reiter's syndrome and Behcet's disease, type I diabetes, Graves' disease multiple sclerosis, pemphigus vulgaris, psoriasis, inflammatory bowel multiple sclerosis, pemphigus vulgaris, psoriasis, inflammatory bowel disease, and acquired immune deficiency syndrome (AIDS). It is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a therapeutic composition comprising a first agent that targets an interleukin-15 receptor (IL-15R) and a second agent that targets an interleukin-2 receptor (IL-2R). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-2000; 2000US-232251P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-SEP-2001; 2001WO-US28612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Fig 1; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interleukin-2 receptor (IL-2R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interleukin-15 receptor (IL-15R) and a second agent that targets an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Therapeutic compositions comprising a first agent that targets an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABK47773
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                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                    page 6 is shown as Seq ID No 2 in Fig 1.
121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
                                    121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
                                                                               61
                                                                                                                 61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                          1 MRISKPHERSISIOCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                            1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-329953/36.
                                                                             EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                       The present sequence referred to as Seq ID No 4 (mutant) on
                                                                                                                                                                                                                                         162; Conservative
                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                      162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Signal_peptide
49..162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Substitution of wild type Gln to Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Substitution of wild type Gln to Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zheng XX;
                                                                                                                                                                                                                                                            100.0%; Score 835; DB 23; 100.0%; Pred. No. 6.2e-86;
                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                      Length 162;
                                                                                                                                                                                                                                                      0; Gaps
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RESULT 3 ABB08335

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autoinmune disease. Diseases include rheunatic disease such as systemic lipus erythematosus, rheunatoid arthritis; type I or type II diabetes; system e.g. Hashimoto's thyroidits, ulcerative colitis, Crohn's disease, multiple sclerosis and myasthenia gravis. The inventive agentes may be used to treat acquired immune deficiency syndrome (AIDS) and for suppressing an immune response in patients who have received an organ, tissue or cell transplant or vascular injury. The agents may be used to expressed by activated or malignant immune cells, but not by resting inmune cells, the agents specifically target those cells that have been and binds the IL-15Ralpha with the same affinity as wild type IL-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    a costinulatory signal transmitted between an antigen-presenting cell and a T cell. The composition of the invention has antirheumatic, uropathic, antiinflammatory, dermatological, antiidiabetic, immunosuppressive, anti-HIV (human immunodeficiency virus), antiarthritic, antipsoriatic, antityroid, neuroprotective, vulnerary, ophthalmological and vasotropic activities. The inventive composition is useful for immune response suppression in patients having an immune disease, particularly an immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of interleukin-15 (IL-15), a cytokine and T cell growth factor encoded by the nucleic acid given in ABA02510. The specification describes a therapeutic composition comprising an agent that targets an IL-15 receptor (IL-15R) and a second agent that inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition for treating immune diseases, especially autoimmune diseases, has agent targeting interleukin-15 receptor and agent inhibits costimulatory signal transmitted between T cell and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigen-presenting cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABA02510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antipsoriatic; antithyroid; neuroprotective; vulnerary; ophthalmological; vasotropic; immune response suppression; autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis; type I diabetes; psoriasis; thyroid; gut, central nervous system; type II diabetes; psoriasis; thyroid; gut, central nervous system; multiple scherosis; myasthenia gravis; AIDS; vascular injury; acquired immune deficiency syndrome; organ transplant; malignant cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAY-2000; 2000US-203801P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antirheumatic; uropathic; antiinflammatory; dermatological; antidiabetic; immunosuppressive; anti-HIV; human immunodeficiency virus; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human interleukin-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABBUBBBB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-089831/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interleukin-15 receptor; IL15R; non-immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maslinski W, Zheng XX, Kim YS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Mature_IL-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor and agent that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lacraz SF;
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AAU77996
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Best Local
The present invention relates to a therapeutic composition comprising a first agent that targets an interleukin-15 receptor (IL-15R) and a second agent that targets an interleukin-2 receptor (IL-2R). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                  Claim 7; Page -; 80pp; English.
                                                                                                        Therapeutic compositions comprising a first agent that targets an interleukin-15 receptor (IL-15R) and a second agent that targets an
                                                                                                interleukin-2 receptor (IL-2R)
                                                                                                                                                            WPI; 2002-329953/36.
                                                                                                                                                                                                                  (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT
                                                                                                                                                                                                                                                   14-SEP-2000; 2000US-232251P
                                                                                                                                                                                                                                                                                                               21-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 149
                                                                                                                                                                                                                                                                             14-SEP-2001; 2001WO-US28612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; interleukin-15 receptor; IL-15R; interleukin-2 receptor; IL-2R; immune response; autoimmune disease; rheumatoid arthritis; psoriasis; Reiter's syndrome; type I diabetes; Graves' disease; multiple sclerosis; inflammatory bowel disease; acquired immune deficiency syndrome; AIDS; transplantation; graft versus host disease; T-cell death; AICD; activation induced cell death; passive cell death; ADCC; CDC; antibody dependent cell-mediated cytotoxicity; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                            WO200222805-A2
                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement directed cytotoxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human IL-15 single mutant (Q149D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU77996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU77996 standard; Protein; 162 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMF1NTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCESAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162;
                                                                                                                                                                                        Strom T, Zheng XX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Signal_peptide
49..162
                                                                                                                                                                                                                                                                                                                                                           /note= "Substitution of wild type Gln to Asp"
                                                                                                                                                                                                                                                                                                                                                                                          /label= Mature_IL-15_single_mutant_(Q101D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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Pred. No. 6.2e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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AAU77997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful in patients having graft versus host disease. The pharmaceutical and in patients having graft versus host disease. The pharmaceutical compositions are useful for promoting T-cell death which includes AICD (activation induced cell death), passive cell death, ADCC (antibody dependent cell-mediated cytotoxicity) or CDC (complement directed dependent cell-mediated cytotoxicity) or CDC (complement directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapeutic composition is useful for suppressing an immune response in a patient where the patient has or is at risk of developing an immune disease, particularly an autoimmune disease such a rheumatoid arthritis, Reiter's syndrome and Behcet's disease, type I diabetes, Graves' disease, multiple sclerosis, pemphigus vulgaris, psoriasis, Inflammatory bowel multiple sclerosis, pemphigus vulgaris,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease, and acquired immune deficiency syndrome (AIDS). It is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytotoxicity). The present sequence representing human IL-15 single mutant (0149D) can be used in a therapeutic composition of the invention. Note: The present sequence is not given in the specification but is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       indexed from the information given on page 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU77997 standard; Protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transplantation; graft versus host disease; T-cell death; AICD; activation induced cell death; passive cell death; ADCC; CDC; antibody dependent cell mediated cytotoxicity; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; interleukin-15 receptor; IL-15R; interleukin-2 receptor; IL-2R; immune response; autoimmune disease; rheumatoid arthritis; psoriasis; Reiter's syndrome; type I diabetes; Graves' disease; multiple sclerosis; inflammatory bowel disease; acquired immune deficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU77997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human IL-15 single mutant (Q156D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
                                                                                                                                                                                                                                      Misc-difference 156
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement directed cytotoxicity.
                                                                                                                                                                    WO200222805-A2
                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                       Peptide
                       14-SEP-2000; 2000US-232251P
                                                                    14-SEP-2001; 2001WO-US28612.
                                                                                                                     21-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 AA;
                                                                                                                                                                                                                    /note= "Substitution of wild type Gln to Asp"
                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                /label= Mature_IL-15_single_mutant_(Q108D)
                                                                                                                                                                                                                                                                                                                  /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.3%; Score 829; DB 23; Leny... - 99.4%; Pred. No. 3e-85; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                               AAR83438
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapeutic composition is useful for suppressing an immune response in a patient where the patient has or is at risk of developing an immune disease, particularly an autoimmune disease such a rheumatoid arthritis neiter's syndrome and Behoet's disease, type I diabetes, Graves' disease, multiple sclerosis, pemphigus vulgaris, psoriasis, inflammatory bowel multiple sclerosis, pemphigus vulgaris, psoriasis, inflammatory bowel disease, and acquired immune deficiency syndrome (AIDS). It is also disease, and acquired immune deficiency syndrome (AIDS). It is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a therapeutic composition comprising a first agent that targets an interleukin-15 receptor (IL-15R) and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page -; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Therapeutic compositions comprising a first agent that targets an interleukin-15 receptor (IL-15R) and a second agent that targets an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-329953/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          second agent that targets an interleukin-2 receptor (IL-2R). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interleukin-2 receptor (IL-2R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytotoxicity). The present sequence representing human IL-15 single mutant (Q156D) can be used in a therapeutic composition of the invention Note: The present sequence is not given in the specification but is indexed from the information given on page 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         compositions are useful for promoting T-cell death which includes AICD (activation induced cell death), passive cell death, ADCC (antibody dependent cell-mediated cytotoxicity) or CDC (complement directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful in patients having received a transplant organ, tissue or cell, and in patients having graft versus host disease. The pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                 02-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                       AAR83438;
                                                                                                                                                                                                                                                                                                                                                                                                                AAR83438 standard; Protein; 162 AA
                                                                                                                                                                                                                                            Interleukin-15; epithelium-derived T-cell factor; T lymphocyte
                                                                                                                                         Peptide
                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                      Human interleukin-15 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
06-APR-1994;
                                        19-OCT-1995.
                                                                              W09527722-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 EDLIQSMHIDATLYTESDYHPSCKYTAMKCFLLELQVISLESGDASIHDTYENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRISKPHLRSISIOCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRISKPHLRSISTOCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVDMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strom T, Zheng XX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
  94WO-US03793.
                                                                                                                                                                 Location/Qualifiers
                                                                                                                         /label= leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 829; DB 2:
Pred. No. 3e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Matches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                      Peptide
                                                                                                                                                                                                        antitumor; virucide.
                                                                                                                                                                                                             Interleukin-15; IL-15; hIL-15; T-cell growth factor;
                                                                                                                         Peptide
                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                               Human IL-15
                                                                                                                                                                                                                                                                                              04-SEP-1995
                                                                                                                                                                                                                                                                                                                                     AAR66927;
                                                                                                                                                                                                                                                                                                                                                              AAR66927 standard; Protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                            121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 SISSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoding mature sinian or human IL-15 polypeptides. The active simian and human IL-15 polypeptides are disclosed in AAR83309 & IL-15, including human IL-15, that hybridise to probes defined by CDMA was deposited with ATCC on Feb. 19 1933 under ATCC 69245. The deposit was named 141-hETF. AAR83408 is a mammalian mature AAR83309 (simian) and AAR83310 (human) IL-15 mature polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 24; Page 28-29; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating carcinoma(s), melanomas, etc. and viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated DNA encoding polypeptide with mammalian IL-15 activity - which stimulates proliferation and differentiation of T cells, used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A simian species of IL-15 (sIL-15) was purified and its AA sequence and cDNA sequence analysed (see AAR83309, AAR83436, AAT00524, AAT00525). Both the simian and the human ORFs encode a precursor polypeptide (AAR83436, AAR83438). The precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT00526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson DM, Eisenman JR, Fung V, Grabstein KH; Rauch C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 EDLIOSMHIDATLYTESDVHPSCKVTANKCFLLELOVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptides each comprise a 48-AA leader sequence and a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRISKPHLRSISIOCYLCLLLNSHELTEAGIHVFILGCESAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRISKPHLRSISTOCYLCLLLNSHFLTEAGIHVFILGCFSAGLÞKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1995-373556/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                        (first entry)
                                    /label= Mat_peptide
/note= "active human IL-15"
                                                                              /label= Sig_peptide
49..162
                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94WO-US03793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 823; DB 16; Length 162; Pred. No. 1.4e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
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PA
XX
PI
PI
DR
DR
DR
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PT
PT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
       08-MAR-1993;
                                                                           US5574138-A
                                        12-NOV-1996
                                                                                                                                Protein
                                                                                                                                                                                                             Cercopithecus aethiops.
                                                                                                                                                                                                                                        HIV infection; human immunodeficiency virus
                                                                                                                                                                                                                                                    SETF: African green monkey: CV1/EBNA cell; T-cell; B-cell; lymphocyte; proliferation; differentiation; gastrointestinal;
                                                                                                                                                                                                                                                                                                          Simian epithelium derived T cell factor precursor
                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                    11-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                AAW09098;
                                                                                                                                                                                                                                                                                                                                                                                                                       AAW09098 standard; Protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A SIL-15 probe was prepared from isolated simian interleukin-15 cDNA and used to screen a cDNA library generated from the IMTLH cell line derived from human bone marrow stromal cells. Clone I41.hETF encoded human IL-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 24; Page 28-29; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New purified interleukin-15 - which induces {\tt T} cell proliferation and differentiation, used for the treatment of tumours and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ84584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-082473/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kauch C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson DM, Eisenman JR, Fung V, Grabstein KH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 EDLTQSMHIDATLYTESDYHPSCKYTANKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-DEC-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZA9402636-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCESAGLPKTEANWUNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
93US-0031399
                                                                                                                             /label= leader
49..162
                                                                                                     /label= mature_serr
                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94ZA-0002636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94ZA-0002636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.6%; Score 823; DB 16; Length 162; 98.8%; Pred. No. 1.4e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Gaps

0;

XX XX ETT

XZZX

AAR66927 RESULT 7 Дb QУ DЬ

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AAW07255
ID AAW0
ID AAW0
XX
AC AAW0
XX
DDT 05-1
DT 05-1
CX
CXX
Epi
KW epi
KW epi
KW prii
KW prii
XX
SX
Hom
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FH Key
FT Pep
FT Pro
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                                                                                                                                                                                                                                                                                                                                                                                                      Db
                                                                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-FEB-1995;
08-MAR-1993;
22-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The simian ETF (epithelium derived T cell factor) was isolated from African green monkey CVL/EBNA cell conditioned medium. The N-African green monkey CVL/EBNA cell conditioned medium. The N-African green monkey CVL/EBNA cell conditioned and then PCR terminal sequence of the purified sETF was determined and then PCR primers were designed based on the sequence information. A 92 by fragment was amplified from CVL/EBNA DNA and was used as a probe to sequence. Mature sETF induces proliferation and/or differentiation of precursor or mature T cells and is useful for promoting long-term of precursor or mature T cells and T-cell lines. It is used for in vitro culture of T-lymphocytes and T-cell lines. It is used for malignancy and for treating HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New epithelium derived T cell factor - induces proliferation of T and B cells, stimulates destruction of tumour and virus-infected cells and protects against toxicity, partic. for treating intestinal disease and HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson DM, Eisenman JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                  Epithelium-derived T-cell factor; simian; human; culture; proliferation;
epithelial cell; differentiation; T-lymphocyte; African green monkey;
primer; PCR; polymerase chain reaction; amplification; probe.
                                                                                                                                                                                                                   Human epithelium-derived T cell factor.
                                                                                                                                                                                                                                                                                       AAW07255;
                                                                                                                                                                                                                                                                                                                        AAW07255 standard; Protein; 162 AA
                                                                                                                                                                                                                                                        05-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                    121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                  Homo sapiens.
                                    Protein
                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 EDLIOSMHIDATLYTESDYHPSCKYTAMKCFLLELQVISLESGDASIHDTYENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASTHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0393305.
93US-0031399.
                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0233606
                                    /note= "signal peptide" 49..162
                                                                                  Location/Qualifiers
                     /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fung V, Grabstein KH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 823; DB 17; Length 162; Pred. No. 1.4e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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AAR98527
                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the amino acid sequence of a human epithelium-derived T-cell factor (ETF). The gene was obtained using a 1.37 kb fragment of the corresp. African green monkey gene (AAT42242) as a probe to screen a corresp. African green monkey gene (AAT42242) as a probe to screen a cDNA library constructed from RNA derived from the LMTHL cell line. This cell line is derived by stable transformation of a human bone marrow stromal cell culture with pSV3neo. From a pool of about 1000 cDNA clones, one clone I41.hETF contained the gene. ETF is a protein of 15-17 kD which is expressed by epithelial cells and stimulates proliferation and/or differentiation of precursor and/or mature T cells. The protein is therefore useful for promoting long term in vivo culture of T-lymphocytes and "-c-ell lines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5552303-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated simian and human epithelium-derived T-cell factors which stimulate the proliferation and/or differentiation of T-lymphocytes and T-cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 21; Column 23-24; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT42243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-412063/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T-lymphocytes and T-cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                       Human interleukin-15
                                                                                                                                                                                                                                                                         AAR98527;
                                                                                                                                                      allograft; T-cell growth factor.
                                                                                                                                                                                                                                           17-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                           AAR98527 standard; Protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
                              Misc-difference 156
                                                                  Misc-difference 56
                                                                                                                    Homo sapiens.
                                                                                                                                                                    Interleukin-15; antagonist; mutein; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                              121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 EDLIQSMHIDATLYTESDVHPSCKVTANKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRISKPHLRSISIOCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRISKPHERSISIOCYLCELLENSHFLTEAGIHVFILGCESAGEPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eisenman J, Fung V, Grabstein K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0031399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93US-0031399.
                /note= "preferred site for amino acid substn."
                                                                                    Location/Qualifiers
                                                  note= "preferred site for amino acid substn."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.6%; Score 823; DB 17; Length 162; 98.8%; Pred. No. 1.4e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
         Protein
                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                     Wild-type interleukin-15 (IL-15).
                                                                                                                                                                                                                                                                                                                                                                07-MAY-1998 (first entry)
                                                                    Peptide
                                                                                                                                                                                                  type l diabetes; AIDS
                                                                                                                                                                                                      Interleukin-15; IL-15; mutant; human; treatment; autoimmune disease;
psoriasis; multiple sclerosis; rheumatic arthritis; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW37369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW37369 standard; Protein; 162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful as antagonists of II-15 and can be prepd. by pCR-mediated mutagenesis of the encoding sequences (see also AAT36543-35). Asp56 and/or Gln156. Asp56 is believed to affect binding to the II-15 receptor beta subunit, and Gln156 to affect binding to the II-15 receptor gamma subunit. By substituting at least 1 of these transduction to cells is prevented while affinity for the II-15 receptor is maintained. The muteins are useful for treating receptor is maintained. The muteins are useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           graft-versus-host disease and for prolonging allograft survival.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antagonists of interleukin-15 - are used to treat patients having symptoms of graft-versus-host disease and for prolonging allo:graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human interleukin-15 (IL-15) (AAR98527) is a T-cell growth factor. Muteins of human IL-15 or simian IL-15 (see also AAR98526) are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 25; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-402367/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
49..162
                  /note= "signal sequence"
                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paxton RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0392317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 823; DB 17;
Pred. No. 1.4e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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T
18-MAR-1997 (first entry)
                                                   AAW01658;
                                                                             AAW01658 standard; Protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dermarcmysitis, polymyositis, Reiter's Syndrome and Behcet's disease. It can also be used to treat Hashimoto's thyroiditis, Grave's disease, multiple sclerosis, myasthenia gravis, encephalomyelitis, a variety of injury. The mutant II-15 can also be used for reducing the viability of a cell that expresses a II-15 receptor. It can also be used to diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a disease treatable with an IL-15 antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cellular events that normally occurs when the wild-type IL-15 specifically binds to a cell surface receptor. The mutant IL-15 is used for suppressing the immune response in a patient. It can be used for treating autoimmune diseases such as rheumatic arthritis, type I diabetes or a rheumatic disease selected from systemic lupus erythematosus (SLE), 5jogran's syndrome, scleroderma, mixed connective tissue disease,
                                                                                                                                                                      121 SLSSNGNVTESGCKECEELEEKNIKEFLOSFVHIVOMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the wild-type interlenkin-15 (IL-15) polypeptide. This wild-type sequence can be mutated at codon positions 149 and 156 to create a mutant IL-15 polypeptide. The mutant polypeptide is at least 90% identical to the wild-type IL-15 and is capable of inhibiting at least one of the
                                                                                                                                                                                                         121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Pages 55-56; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutant interleukin 15 polypeptide(s) - used for treating auto-immune diseases e.g psoriasis, multiple sclerosis etc.
                                                                                                                                                                                                                                           61 EDLIGSNHIDATLYTESDVHPSCKVTANKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-APR-1996;
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                                                                                                                                                                                                                                                                                                                         1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-1997.
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                                                                                                                                                                                                                                                                                                                                                              1 MRISKPHLRSISIOCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "The specifications claims a substitution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "mature IL-15 polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                             98.6%; Score 823; DB 18; 98.8%; Pred. No. 1.4e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gln at this position to Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gln at this position to Asp"
                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 162;
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   RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IL-15; interleukin-15; T-cell growth factor; proliferation; stimulate; muscle growth; differentiation; hypertrophy; treat; atrophy; wasting; skeletal; cardiac; muscle; congestive heart failure; diabetes-associated;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glucose-intolerance; dyslipidaemia; rhabdomycosarcoma; dystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human interleukin-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for treating atrophy, or wasting, in particular, skeletal and cardiac muscle atrophy. The compsns. further comprises a steroid, growth hormone and insulin-like growth factor. Congestive heart failure, muscle wasting and diabetes-associated glucose-intolerance or dyslipidaemia, rhabdomycosarcoma and muscular dystrophy can all be treated by such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAT58404.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-NOV-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is human interleukin-15 (IL-15), a known T-cell growth factor that can support proliferation of an IL-2-dependent cell line, CTLL-2. Compsns. contg. IL-15 to stimulate muscle growth, differentiation or hypertrophy are claimed. The stimulation of muscle growth is useful or hypertrophy are claimed. The stimulation of muscle growth is useful or hypertrophy are claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muscle trophic compsn. contg. interleukin 15 - for treating, e.g. congestive heart failure, muscle wasting etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 12; 22pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             compsns
                                                                                                                                                 AAW53878;
                                                                                                                                                                                  AAW53878 standard; Protein; 162 AA
                                cytokine; growth factor
                                                                                Human interleukin-15.
                                                                                                                   13-JUL-1998 (first entry)
Homo sapiens
                                                                                                                                                                                                                                                               121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                             121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
                                                                                                                                                                                                                                                                                                                              61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                            61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1997-020939/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160;
                                                  interleukin-15; IL-15; T cell; B cell; proliferation; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Troutt AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 823; DB 18; Length 162; Pred. No. 1.4e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5747024-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunogenicity augmenting amount of II-15. The composition is useful for enhancing the immunogenicity of a vaccine. The cytokine II-15 is a potent enhancing the immunogenicity of a vaccine. The cytokine II-15 is a potent and B cell growth factor. It causes proliferation and differentiation of these cells and augments T cell mediated immune responses. The vaccine composition can sufficiently elicit an immune response without being deleterious to the recipient, especially when using pathogenically deleterious to the recipient, especially when using pathogenically deficient antigens. Some vaccines do not elicit a strong immune response and cannot provide sufficient protection on further exposure to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-1993;
22-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grabstein KH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use of Interleukin-15 - to enhance immunogenicity of a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-ՄՄԼ-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Column 5-6; 5pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the vaccine of the invention. The vaccine composition immunogenic amount of a vaccine antigen (Ag) and an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is human interleukin-15 (IL-15), which can be used in the vaccine of the invention. The vaccine composition comprises an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                               Simian epithelium derived T-cell factor protein.
                                                                                                                                                                                                                                       AAW39185;
                                                                                                      B-cell stimulation; epithelium; villi; CD4+; CD8+; T-cell stimulation;
                                                                                                                           Epithelium derived T-cell factor; ETF; simian; gastrointestinal disease;
                                                                                                                                                                                                       08-MAY-1998
                                                                                                                                                                                                                                                                            AAW39185 standard; Protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                  121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVOMFINTS 162
Peptide
                                                      Simian.
                                                                                      treatment; prevention
                                                                                                                                                                                                                                                                                                                                                                                                     121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EDLIQSMHIDATLYTESDVHPSCKVTANKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRISKPHLRSISIOCYLCLLLNSHFLTEAG1HVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1998-285678/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-0031399.
94US-0233606.
95US-0393305.
                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0504042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Widmer MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-0504042
      Location/Qualifiers 1..48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 823; DB 19; Length 162; pred. No. 1.4e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                        Qγ
                                                                                                                                                                                                                                                                                                                                                                                                         Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 160;
Epithelium-derived T-cell factor; ETF; immunoassay; enteritis; ulcer; T cell proliferation; gastrointestinal disease; mucositis; colitis; gastroenteritis; villus atrophy; malignancy; inflammatory bowel disease; human immune deficiency virus; tumour; simian.
                                                                            Simian epithelium-derived T-cell factor (ETF) precursor polypetide.
                                                                                                                        10-JUN-1999 (first entry)
                                                                                                                                                                                AAY03756 standard; Protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       radiation-therapy induced enteritis (gut toxicity), mucositis, peptic ulcer disease, gastroenteritis and colitis, villus attrophic disorders, malignancy and inflammatory bowel disease. Eff polypeptides may also be useful in the treatment of human immunodeficiency virus (HIV) and HIV-associated disease due to their ability to stimulate CD4+ and CD8+ dells. Biologically active ETF may be used to treat a variety of other diseases or conditions where T-cell or B cell stimulation is desired.
                                                                                                                                                                                                                                                           121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                         121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a full length simian epithelium-derived T-cell factor (ETF) which is used in a method for treating or preventing gastrointestinal disease. These polypaptides have particular application in the treatment of gastrointestinal disorders associated with disruption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the gastrointestinal epithelium or villi such as chemotherapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Column 35-38; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   administering epithelium-derived T-cell factor polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treatment or prevention of gastrointestinal diseases - by
                                                                                                                                                                                                                                                                                                                     61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAV02873
                                                                                                                                                                                                                                                                                                                                                   61 EDLIQSMHIDATLYTESDYHPSCKYTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5707616-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                 1 MRÍSKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                    1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1998-100295/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       950S-0393305.
930S-0031399.
940S-0233606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eisenman JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0726817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= leader sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= ETF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.6%; Score 823; DB 19; Length 162; 98.8%; Pred. No. 1.4e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fung V, Grabstein KH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disruption
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC antibodies are used, optionally when immobilized or labeled, to detect can dynamity ETF in standard immunoassays. They may also be used as the control of their precursors) or radionuclides. ETF induces proliferation and/or cestablishing long term in vitro cultures; and is also used to treat constitution of T cells (or their precursors). e.g. for use in cestablishing long term in vitro cultures; and is also used to treat constitution of T cells (or their precursors). e.g. for use in cestablishing long term in vitro cultures; and is also used to treat constitution of T cells (or their precursors). e.g. for use in constitution of T cells (or their precursors). e.g. for use in constitution to the constitution of the constitution of T cells (or their precursor) and is also used to treat constitution and inflammatory bowel disease), to treat constitution and immunory and inflammatory bowel disease, or constitution and situation requiring stimulation of T or B cell increased anti-infections disease immunity, induction of T-cell lytic control of constitutions or certain cytokines.

CC activity or increased destruction of tumour or virus-infected cells. The XXX present sequence represents a simian ETF precursor polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                       121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated antibody that binds specifically to a similar or human epithelium-derived T-cell factor (ETF) polypeptide. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Columns 35-36; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibodies specific for epithelium-derived T-cell growth factor
                                                                                                           61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAX29479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-253930/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anderson DM, Eisenman JR, Fung V, Grabstein KH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                              04-OCT-1996;
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22-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                 Match 98.6%; Score 823; DB 20; Length 162; Local Similarity 98.8%; Pred. No. 1.4e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 AA;
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0725969
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Search completed: February 20, 2003, 16:28:23

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Job time : 34 secs

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Result
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Copyright (c) 1993 - 2003 Compugen Ltd.
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interleukin-15 - m
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hypothetical prote

RESULT 2 149124 interleukin-15 - mouse C;Species: Mus musculus (house mouse) C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 16-Jul-1999 C;Accession: 149124 R;Anderson, D.M.; Johnson, L.; Glaccum, M.B.; Copeland, N.G.; Gilbert, D.J.; Genomics 25, 701-706, 1995 A;Title: Chromosomal assignment and genomic structure of Il15. A;Reference number: A56005; MUID:95278940; PMID:7759105 A;Scatus: preliminary A;Molecule type: mRNA	RESULT 1 A53484 interleukin-15 precursor - green monkey C:Species: Cercopithecus aethiops (green monkey, grivet) C:Apecies: Cercopithecus aethiops (green monkey, grivet) C:Bate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, K.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, M.H.: Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fu R:Grabstein, J.; Shane	ALIGNMENTS	30 76 9.1 468 2 T52418 cytochrome p450 - 31 76 9.1 725 2 H96989 cdcl0 start control 32 76 9.1 1767 1 COZPCD 33 76 9.1 1790 2 G84982 exodeoxyribonucles 34 76 9.1 1790 2 G87593 transport protein 35 75.5 9.0 521 2 JC5505 DNA helicase Q1 in 36 75.5 9.0 729 2 A49120 37 75.5 9.0 1353 2 T1991 hypothetical prote 39 75 9.0 307 2 B38448 40 75 9.0 307 2 B38448 40 75 9.0 307 2 C97303 hypothetical prote 40 75 9.0 849 2 C97303 hypothetical prote 41 75 9.0 849 2 C97303 hypothetical prote 42 75 9.0 1021 2 T42634 connectin/fitin - 43 74.5 8.9 365 2 B40896 Ca2+Calmodulin-de 45 74.5 8.9 572 2 T28177
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A;Cross-references: EMBL:U14332; NID:g984941; PIDN:AAA75377.1; PID:g984942
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C; Superfamily: interleukin-15
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A.Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: H97846
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R;Ouellette, F.; Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, B.; Fortin, N.; submitted to the EMBL Data Library. January 1993 A;Description: Sequencing of Chromosome I from Saccharomyces cerevisiae: analysis of a A;Reference number: S36711
                                                                                                                        FUN26 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YALD22c
C;Species: Saccharomyces cerevisiae
C;Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 29-Oct-1999
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 29-Oct-1999
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C;Date: 21-Jan. -. C;Date: 21-Jan. -. C;Accession: T28168
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R;Afonso, Ct.L; Tulman, Ct.L;Tulman, 
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A;Molecule type: DNA
A;Residues: 1-517 < OUE>
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F:177-193/Domain: transmembrane #status predicted <TM3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein ORF8 - Melanoplus sanguinipes entomopoxvirus (isolate Tsucon) C;Species: Melanoplus sanguinipes entomopoxvirus A;Variety: isolate Tuscon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: The genome of Melanoplus sanguinipes entomopoxvirus A;Reference number: 220484; MUID:99102612; PMID:9847359 A;Accession: T28168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AF063866; NID:g4049647; PIDN:AAC97859.1; PID:g4049899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-500 <AFO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: isolate Tuscon
                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                       200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403 DQKETPRKTFIYSLLRVAAIPLELMFTAITSSSSGDEEHNGSV--IVDLCYMLLQELEGV 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461 TNGHVISMSFMKVPEQLDNDDEKEAAGGFTNI---FVST 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 SNGNV-TESGCKECEELEEKNIKEFLDSFVHIVDMFINT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 YLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKIEDLIQSMHIDATLYT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 ESDVHPS-----CKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS----- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                            149 NECKII-DFKFLESLINLEILDVSYNKNSNIYECTLPISLIELKCISCKIIDFKFLESLI 207
129 TESGCKECEELEEKNIK-----EFLDSFVHIVDMFINTS 162
                                                                                208 NLETLDVSSNEYSNISDCKLPVSLIKLNCEFCYTYDFKFLETLNNIKIL-NISYNKNSNI 266
                                                                                                                                                                                                                                                                                                                            49 NWVNVISDLKKIEDLIQSMHIDATLYTESDVHP-----SCKVTAMKCF--LL 93
                                                                                                                                                                                                                                                                                                                                                                                                       90 TYKCKLSSLLKNLNCNECKTIDEKFL-ESLINLETLDISYNKNSNTYKCKLSSLLKNLNC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                           94 ELQVISLESGDAS------IHD-----TVENLIILANNSLSSNGNV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 10.4%; Score 86.5; DB 2; Length 500; Local Similarity 21.8%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ISKPHLRSI--SIQCYLCLLLNSHFLTEAGIHVFILG------C-FSAGLPKTEA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tulman, E.R.; Lu, Z.; Cma, E.; Kutish, G.F.; Rock, D.L. 33-552, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative 42: Mismatches 61; Indels 73; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.5%;
25.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 96; DB 2
Pred. No. 0.57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>ن</u>
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A:Gene: trps; Cj038
C:Superfamily: tryp
C:Keywords: ligase
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A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-319 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypersection: B81382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling, C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre, Nature 403, 665-668, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tryptophan-tRNA ligase (EC 6.1.1.2) Cj0388 [imported] - Campylobacter jejuni (strain NCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: nad2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Genome: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Cross-references: EMBL:U02970; NID:9467843; PID:9467875; PIDN:AAD12662.1
                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Status: preliminary: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Wolff, G.; Plante, I.; Lang, B.F.; Kueck, U.; Burger, G.
J. Mol. Biol. 237, 75-86, 1994
A;Tille: Complete sequence of the mitochondrial DNA of the chlorophyte alga Prototheca
A;Reference number: 217373; MUID:94180393; PMID:8133522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Prototheca wickerhamii mitochond C:Species: mitochondrion Prototheca wickerhamii
C:Date: 16-Jui-1999 #sequence_revision 16-Jui-1999 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ъ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                     262 ----FKIYLNELV--NAYFKEAREKYNELLEKPSHLKEILD 296
                                                                                                                   109 DTVENLIILANNSLSSNGNVTESGCKECEELEE-KNIKEFLD 149
                                                                                                                                                             202 SSEKTLKKQISSIVTDSTALEDPKDHENCNIFKIAKLFLDESGQKELQIRYEKGGEGYGH 261
                                                                                                                                                                                                                                                        142 VGKDQIQHVEIARDIALKVNNEWGEIFTLPEARVNEEVAVVVGTDGAKMSKSVQNTIDIF 201
                                                                                                                                                                                                           55 SDLKKIEDLIOSMHIDATLYTESDVHPSCKVTAM-KCFL----LELQVISLESGDASIH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 LQSLSFYVLAALKRNSEFATEAGLKYFLLGAFSSGL 192
                                                                                                                                                                                                                                                                                                         3 ISKPHLRSISI@CYLCLLLNSHF-----LTEAGIH----VFILGCFSAGLPKTEANWVNVI 54
                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            trps; Cj0388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 LRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGL 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 S-----DCKKLPVSLIKLNCGYCYIYDFKFLEPLINLQKLNISSN 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .-510 <WOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tryptophan-tRNA ligase
                                                                                                                                                                                                                                                                                                                                                      Conservative 33; Mismatches 68; Indels 22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 10.18;
24.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.2%;
                                                                                                                                                                                                                                                                                                                                                                                         Score 84; DB 2; Length 319; Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 85;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 510,
                                                                                                                                                                                                                                                                                         A:Description: involved in atrazine degradation [validated, MUID:96011356] C:Superfamily: Aquifex aeolicus N-ethylammeline chlorohydrolase
                                                                                                                                                                                                                                                                                                                                                                    C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:L16534; NID:g294669; PIDN:AAA90931.1; PID:g294671
A;Experimental source: tissue lib NRRL 15444B
                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: trzA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-477 <SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: T46666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: Z23125; MUID:96011356; PMID:7592318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Cloning and expression of the s-triazine hydrolase gene (trzA) from Rhodococ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: s-triazine hydrolase C;Species: Rhodococcus corallinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Shao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-ethylammeline chlorohydrolase [validated] - Rhodococcus corallinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DЬ
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                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Introns: 51/2;
A;Note: T4F9.30
                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \underline{\underline{A}}: Experimental source: cultivar Columbia; BAC clone T4F9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-928 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K submitted to the Protein Sequence Database, March 1999 A;Reference number: Z15260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AL049523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999 C;Accession: T04192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T4F9.30 - Arabidopsis thaliana N;Alternate names: protein T4F9.30 C:Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
381 IGSLEAGKRADIITLDLRHAQTTPAHDLAATIVFQAYGNEVNDVLVNGSV 430
                                                                                             321 TVGIGTDDANCNDSVNLISDMKVLALIHRAAHRDASIITPEKIIEMATIDGARCIGMADQ 380
                                                97 VISLESGDAS------IHDTVENLIILAN----NSLSSNGNV 128
                                                                                                                                           40 SAGLPKTEANW----VNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTANKCFLLELQ 96
                                                                                                                                                                                                                        Match 9.9%; Score 82.5; DB 2; Length 477; Local Similarity 23.6%; Pred. No. 8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 SIVTIAGGPTLSNGHSTTS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 NLTILANNSLSSNGNVTES 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 DPLSYKSLEE--SSLHMDQDILVEVDGLSSSSQSAMSSTGNELALVPLEPS-----R 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 YTRSYSVEVYPLÖLMLTDGRDESRTASIRELYEKVCAMTGVPQEKAHIMDYFDKRKNGLL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 D---LKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z.Q.; Seffens, W.; Mulbry, W.; Behki, R.M.
riol. 177, 5748-5755, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 HLRSISIQCY-LCLLL---NSHFLTEAGIHVFILGCFSAGLPKTEAN-W-----VNVIS 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51/2; 122/2; 161/3; 181/3; 214/3; 328/1; 401/3; 458/3; 544/3; 596/2; 774/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36; Conservative 25; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 10.1%; Score 84; DB Similarity 25.9%; Pred. No. 14;
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                              22; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 928;
                                                                                                                                                                                           Gaps
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B ΩУ В 0γ Db

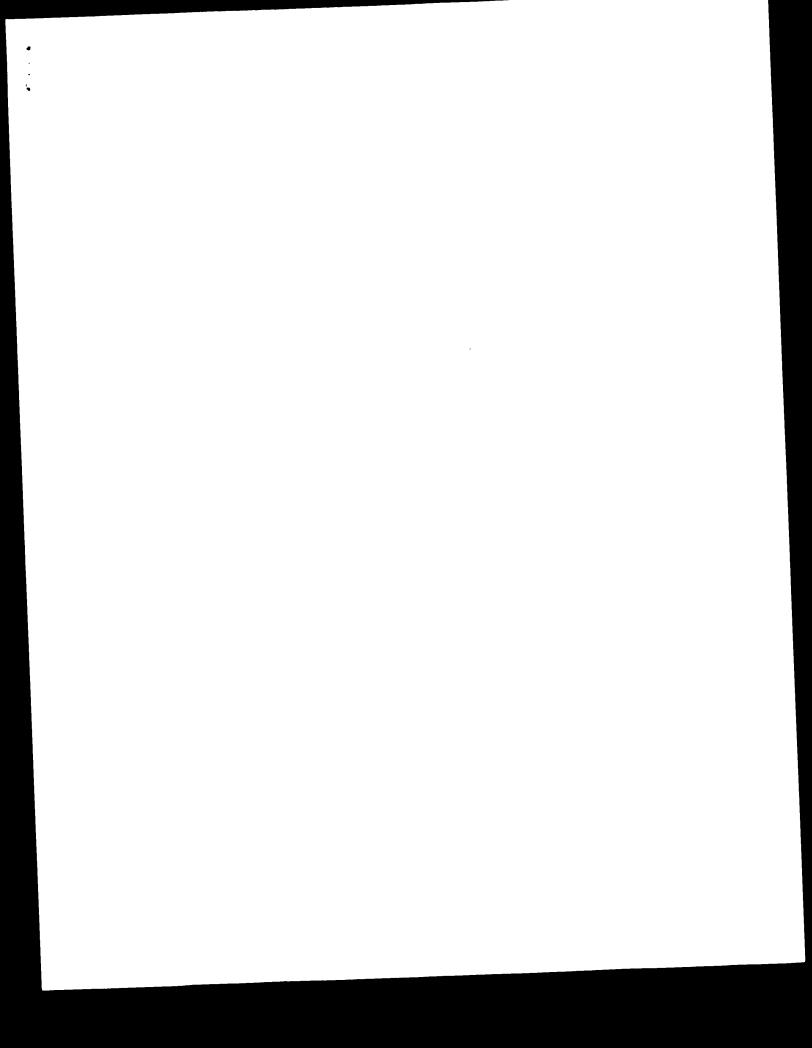
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RESULT 10
AD1895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Nostoc Sp. A;Note: Nostoc Sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 A;Note: Nostoc Sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 A;Note: Nostoc Sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And A;Teference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD1895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguc
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             serine/threonine kinase with two-component sensor domain air0710 [imported] - Nostoc sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1799 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB72667.1; PID:g17130055; GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A: Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: alr0710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:MOTTOW, B.B.; Ju, Q.; Warner, J.R.
MO1. Cell. Biol. 13, 1173-1182, 1993
MO1. Cell. Biol. 13, 1173-1182, 1993
A:Title: A bipartite DNA-binding domain in yeast Reblp.
A:Title: A bipartite AR8077; MUID:93140755; PMID:8423784
A:Accession: A48077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myb-related protein REB1 - yeast (Kluyveromyces marxianus var. lactis)
C:Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вр
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:L03789; NID:g173313; PIDN:AAA61343.1; PID:g173314
A;Cross-references: GB:L03789; NID:g173313; PIDN:AAA61343.1; PID:g173314
A;Note: sequence extracted from NCBI backbone (NCBIN:123574, NCBIP:123576)
A;Note: sequence extracted from NCBI myb DNA-binding repeat homology
C;Superfamily: myb-related protein REB1; myb DNA-binding regulation
C;Keywords: DNA binding; nucleus; transcription regulation
C;Keywords: DNA binding repeat homology (MYB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: A48077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-595 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
   B
                                                     QΥ
                                                                                                                     B
                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1669 NYGDLPLVNCFPGOLNQVFMNILANAIDALEEANIGKSFAEITAHPNRITITTS 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1609 AMINACURLENISTSLRTFSRADKDYKVKFULHEGIDSTILILKHRLKANQOHPAIEVIT 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 --GNVTESGC------KECEELEEKNI-KEFLDSFVHIVDMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 LGCESAGLPKTEANWVNVISDLK-----KIEDLIQSMHIDATLYTESDVHPSCK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 VTAMKCFLLE-----LQVISLESGD----ASIHDTVENLIILANNSLSSN------ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
235 NDDQQDDVSNLIQEAAAKASHIINPATQSNGKSFDESEEEALEQFIKEYQKI 286
                                                        104 DASIHDTVENLIILANNSLSSNGN-VTESGCKECEELEEKNIKEFLDSFVHI 154
                                                                                                                        183 PKKEKSEERSYGDLSNIDDHVDDVSVSGSIPSQVRLKKTAEVLP-----KVLSSESH 234
                                                                                                                                                                                 44 PKTEANWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESG 103
                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h
Similarity 22.4%; Score 82; DB 2; Length 1799;
                                                                                                                                                                                                                                                    28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                  9.8%; Score 81.5;
25.0%; Pred. No. 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27; Mismatches
                                                                                                                                                                                                                                                              23; Mismatches
                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                              DB 1; Length 595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58; Indels 50; Gaps
                                                                                                                                                                                                                                                                     52; Indels
                                                                                                                                                                                                                                                                               9;
                                                                                                                                                                                                                                                                                  Gaps
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submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid R03H4.
A;Reference number: Z20534
A;Accession: T28866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein R03H4.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 35/2; 66/2; 123/3; 166/3; 280/3; 321/1; 419/3; 460/1; 495/2; 586/3 C;Superfamily: Caenorhabditis elegans hypothetical protein T26H2.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U50300; PIDN:AAC48109.1; GSPDB:GN00023; CESP:R03H4.1 A;Experimental source: strain Bristol N2; clone R03H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-642 <BRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Status; preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP:R03H4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Geisel, C.; Kramer, J.; Smith, A.; Elliott, G.; O'Brien, submitted to the EMBL Data Library, July 1997 A;Description: The sequence of C. elegans cosmid C02A12. A;Reference number: Z16067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein CO2A12.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-922 <WIL>
                                                                                                                                                                                                                                                                                                             A; Introns: 35/2;
A; Note: C02A12.2
                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:AF016415; NID:g2291123; PIDN:AAB65265.1; PID:g2291126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: T03854
                                                                                                                                                                                                                                                                                                                                                      A; Map position: V
                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                        ν
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
9
                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  517 NIQFYESIAKKIYILGSH----PLYNINHLNTFLHYLIQNSDELESLHLNR---FKSDDD 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              570 MRCVKKRPEKVKCKKCOPFDLSHVEVE-GDKYLTFDRDSLISYVDNTI----HLTSAGLK 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              625 LCQPVFENLAKEIMNN 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 ECEELEEKNIKEFLDS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 PSC-----KVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 NSHFLTEAGIHVFILGCFSAGLPKTEANWVNV-ISDLKKIEDLIQSMHIDATLYTESDVH 80
                                                                                                                                  543 VFILG----ALPTYPVNFLNAFLQNVMKSQEDMEKLHLNQKT-ADEDVKNEVKRFELAEK 597
                                             598 RCK----KCQFIDLNPAFLEKGKYLTFD--RNSLL---SYLDNSGHLMPAAVKLCEPILE 648
    142 KNI 144
                                                                                      82 SCKVTAMKCFLLELOVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEE 141
                                                                                                                                                                             33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T28866
                                                                                                                                                                                                                                                                                                                                   35/2; 66/2; 123/3; 179/3; 290/3; 331/1; 434/3; 475/1; 510/2; 603/3; 658/2;
                                                                                                                                                                                                                              Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.8%; Score 81.5; DB 2; 24.3%; Pred. No. 16;
                                                                                                                                                                                                                                                      9.6%;
25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28; Mismatches 56;
                                                                                                                                                                                                                                                        Score 80.5;
Pred. No. 30
                                                                                                                                                                                                                                                               30;
                                                                                                                                                                                                                                                                                     DB 2; Length 922;
                                                                                                                                                                                                                                          43; Indels 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 19; Gaps
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Db 649 KTI 651
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Qγ C:Superfamily: X-Pro aminopeptidase R;Takami, H.; NakaSone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A:Reference number: A83650; MUID:20512582; PMID:11058132 A:Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB06898.1; GSPDB:GN00 A:Molecule type: DNA A:Residues: 1-364 <STO> C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 Prolidase (proline dipeptidase) pepQ [imported] - Bacillus halodurans (strain C-125) RESULT 15 Qγ Qy Matches Дb Query Match A:Map position: 4 A:Introns: 1/3; 26/3; 66/3; 80/2; 151/1; 745/3; 786/3; 976/3; 1045/1; 1120/1; 1155/3; 12 A;Residues: 1-1817 <BEV>
A;Cross-references: EMBL:AL049915; GSPDB:GN00062; ATSP:T16118.30
A;Experimental source: cultivar Columbia; BAC clone T16118 A; Gene: ATSP:T16I18.30 R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancrq Submitted to the Protein Sequence Database, June 1999 hypothetical protein T16I18.30 - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Datte: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999 A:Molecule type: DNA A; Accession: T10689 RESULT 14 Best Local Similarity 59 KIEDLIQSMHIDATLYTES-----DVHPSCKVTAMKCFLLELQVISLESGDASIHDTVE 112 37 PHERLYSLLLFPEAEPCLICPNMETSLVKEAGWTGEIL-----GYSDIEDPWLLVRQAVE 91 Local Similarity 6 PHLRSISI------OCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLK 58 750 SQNADGIEEEKKSCFLDAAI 769 133 CKECEELEEKNIKEFLDSFV 152 690 LQVLLDSTGTGESVVTPKTSSKNSSESWDHLVAEEVKAILLCISQVKNSLDQSGNSRYSD 749 645 LPAYAVKTEEGISSV--ELSALEVLIKACOKSKPIDVEVY-----MNCHRRK 689 585 IORPHCRRVRELTINRIIHEINLLKIDELLENNIPEMMEKEEYSECVNLLAPLLEPDKDI 644 95 LOVI----ANNSLSSNGNVTESG 132 45 -----KTEANWVNVISDLKKIEDLI----QSMHIDATLYTESDVHPSCKVTAMKCELLE 94 3 ISKPHLR-----SISIOCYLCLLLNSHELTEAGI-----HVFILGCESAGLP------ 44 36: Conservative .ch 9.6%; Score 80.5; DB 2; Length 1817; Ll Similarity 23.5%; Pred. No. 67; 47; Conservative 25; Mismatches 63; Indels 65; Gaps 9.5%: Score 79.5; DB 2; Length 36 22.4%: Pred. No. 12; ative 29; Mismatches 67; Indels DB 2; Length 364; 29; Gaps 8

Search completed: February 20, 2003, 16:32:08 Job time: 26.5 secs



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Post-processing: Minimum Watch 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
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Maximum DB seq length: 20000000000
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Sequence:
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                                   Score
                                958.6
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1 MRISKPHLRSISIQCYLCLL.....NIKEFLDSFVHIVDMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               February 20, 2003, 16:27:07; Search time 16.5 Seconds (without alignments) 407.222 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SwissProt_40:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                          IMA4_HUMAN
FGR1_DROME
LXD2_PHOLU
CDAA_HUMAN
                                                                                                                                            GLMS_PYRAB
USO1_YEAST
YJ9C_YEAST
ADB6_YEAST
ADB6_YEAST
NU2M_ACACA
CPCJ_HUMAN
HSF1_CHICK
CC10_SCHPO
EX5C_BUCA1
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REB1_KLULA
TRPA_BUCSC
RINI_RAT
HCYG_SEPOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL15_MACMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                          p38529 gallus gall
P01129 schizosacch
P57528 buchnera ap
000629 homo sapian
007407 drosophila
P23148 photorhabbu
099512 homo sapian
P22517 saccharomyc
                                                                                                                                                                                                                               p31381 Saccharomyc
Q52725 rhodococcus
Q52725 rhodococcus
Q5950 kluvveromyc
Q4404 buchnera ap
p23315 rattus norv
p56826 sepia offic
Q94048 candida alb
Q9v249 p glucosami
p25386 saccharomyc
P47166 saccharomyc
                   Q94655
Q03018
Q02099
                                                                                                                                                                               P47166 saccharomyc
P46582 saccharomyc
Q37376 acanthamoeb
P33261 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                       P40933 homo sapien
P48092 macaca mula
P40221 cercopithec
O97687 felis silve
                                                                                                                                                                                                                                                                                                                                                                                        Q95253
Q28028
Q9xsj6
P48346
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                                                                                                                3 buchnera ap
9 homo sapien
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                                saccharomyc
                                             plasmodium
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bos taurus
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mus musculu
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         SEQUENCE OF 49-162 FROM N.A.
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Result

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Searched:

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SEQUENC: TISSUE=: MEDLINE MEAZZA I OZENGO I Identi Generat Concogene [4] SEQUENCE TISSUE-T MEDLINE-T MEDLINE-T MEDLINE-T MEDLINE-T TAGAYA Y TAGAYA Y TAGAYA Y TOGAYA TOGANGA "Generat through, Proc. Na [5] SEQUENCE MEAZZA R "EXPRESS: COrrelatts Correlatts		RESULTILLS_H	440000
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SEQUENCE FROM N.A. (IL15-S21AMEDLINE-96218668; PubMed=8668 Meazza R., Verdiani S., Biasso Orengo A.M., Colombo M.P., Azz Grengo A.M., Colombo M.P., Colo	CCE FROM E=94233; ein K.K. asan S., M., Joh G.; interle 264:96 EFROM H., Jan Stein T.	HUMAN 3; Q9305 3-1995 (3-1995 (1-2001 (-eukin-1 -eukin-1 -eukin-1 -eukin-1 -eukin-1	74 73.5 73.5 73.5 73.7 73.5 72.5 72.5 71.5 71.5
Pul boo a a nai 192 192 (J	SEQUENCE FROM N.A. (IL15-S48 TISSUE-Bone marrow; MEDLINE-94233380; pubMed=817 Grabstein K.K., Eisenman J., Srinivasan S., Fung V., Beer Ahdieh M., Johnson L., Alder Giri J.G.; "Cloning of a T cell growth of the interleukin-2 recepto Science 264:965-968(1994). SEQUENCE FROM N.A. (IL15-S48) Krause H., Jandrig B., Wernic Submitted (SEP-1995) to the	JULT 1 1.15_HUMAN TI.15_HUMAN TI.15_HUMAN TI.15_HUMAN STANDARD; PAT; P40933; 093058; 043512; 000440; 09UBA 01_FEB-1995 (Rel. 31, Last sequence u 16-OCT-2001 (Rel. 40, Last annotation Interleukin-15 precursor (IL-15). IL15_HOMO Sapiens (Human). Eukaryota: Metazoa: Chordata; Craniat. Mammalia; Eutheria: Primates; Catarrh NCBLTaxID=9606;	8.000000000000000000000000000000000000
IL15-S2 bMed=86 S. Bia M.P., novel tive sp 2(1996) 2(1996) 2(115-S2: LL15-S2: Thies 7 Thies 7 n T.A.; able an	(ILI5-S48A) ubMed=8178 eaman J., V., Beers L., Alders 1 growth f. 2 receptor (1994). (ILI5-S48A) to the Ex	DARD; 512; 00 1, Crea 1, Last 0, Last ursor (ursor (Chorda:	668 938 521 521 521 497 4393 791 807 364 356 456
88668345; ilassoni Azzaro interla splicing 6). S2lAA ISC S2lAA ISC S2lAA ISC 9405632; T.A., I A., I A.		00044 bated it se t an (IL- (IL-	
AA ISOFORM 3345; soni R., Co zarone B., tterleukin cing in hu cing	IS 55; hea hea cto cto pto IS IS	PRT 0; Q 0); Q iquen nota nota 15), Crar	V244_I V120_I IMA3_I IMA3_I IMA3_N PGBM_I LON_GA PTNM_H PYRC_Y PYRC_Y PYRC_Y RINI_P RINI_P RINI_P
AA ISOFORM). 8345; soni R. Coppol scarone B. Fer terleukin-15 (cing in human (cing in human). A ISOFORM). 632; A., Losi J.M., nonsecretable gnal peptides " 94:14444-14449		PRT; 16; QUBA3; QUBA3; uence upd otation u; 5).	V244_FOWPV V120_HSV7J V1A3_HUMAN V1A3_HOUSE NU2M_CHOCR NU2M_CHOCR NU2M_CHOCR NU2M_CHOCR NU2M_CHOCR NU2M_CHOCR NU2M_CHOCR NU2M_CHOCR NU3M_HUMAN LONGLE PTML HUMAN RINI_PIG ALIGNMENTS
ecchia M., rini S.; IL-15) tran cell cell cell cell small cell Azimi N., azimi N., interleuki	R., Rauch C dson J., Sc tson J.D., interacts w interacts w	2 AA. ate) pdate) vertebrata; E	TTS
ggerc ript ng ca nover	M. D. D.	leos	Q9j4z6 P52438 Q005344 C35344 P48903 P98160 Q6932r2 Q92051 Q920651 Q920651 Q92051 P30550 P10775
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us-09-855-313a-2.rsp

Submitted

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SUBCELLULAR IS NOT
SUBCELLULAR IS STORED INTRACELLULARLY, APPEARING IN THE
SECRETED, BUT RATHER IS STORED INTRACELLULARLY, APPEARING IN THE
NUCLEUS AND CYTOPLASMIC COMPONENTS.
NUCLEUS AND CYTOPLASMIC COMPONENTS.
ALTERNATIVE PRODUCTS: 3 ISOFORMS; IL15-S48AA (SHOWN HERE),
IL15-S21AA AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: MOST ABUNDANT IN PLACEMTA AND SKELETAL MUSCLE.
IT IS ALSO DETECTED IN THE HEART, LUNG, LIVER AND KIDNEY. IL15IT IS ALSO DETECTED IN THE HEART, LUNG, LIVER AND STESTIS AND
S21AA IS PREFERENTIALLY EXPRESSED IN TISSUES SUCH AS TESTIS AND

Sorel M.A., Jacques Y.; "IL15 expression in hum TISSUE=Epidermis;

in human keratinocytes.";

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IL15_MACMU
                                                Дb
                                                                      QУ
                                                                                              Db
                                                                                                                     QΥ
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P48092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last anotation update)
                                                                                                                                                                     Query Match
                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interleukin-15 precursor (IL-15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Comparative sequence analysis of cytokine genes from human and nonhuman primates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96003435; PubMed=7561102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         EMBL; U19843; AAB60398.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
                                                                                                                                                                                                                                                                                                                        Pfam; PF02372; IL15;
                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                      PROPEP
                                                                                                                                                                                                                                                                                                           Cytokine; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immuno1.
121 ILSSNGNITESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                        121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
                                                                          61
                                                                                                                                                           Match 95.8%;
Local Similarity 95.1%;
                                                61 EDLIQSMHIDATLYTESDVHPSCKVTANKCFLLELQVISHESGDTDIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAMMA BUT NOT IL-2R ALPHA.
                                                                                                              1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWYNVISDLKKI 60
                                                                                                MRISKPHLRSVSIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                         EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                               AB000555; BAA19149.1;
                                                                                                                                                   154;
                                                                                                                                                                                                                                                                                                                                    IPR003443; Interleukin_15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155:3946-3954(1995).
                                                                                                                                                                                                     162 AA;
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83
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127
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                                                                                                                                                   Conservative
                                                                                                                                                                                                     18194 MW;
                                                                                                                                                                                                                                                                                                                   Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mayne A.E., Chikkala N., Ansari A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                       2; Mismatches
                                                                                                                                                                 Score 800; DB 1;
Pred. No. 2.4e-65;
                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                     I -> T
                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                              INTERLEUKIN-15.
                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                        D233CF7FF6188C01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 AA
                                                                                                                                                                                  DB 1; Length 162;
                                                                                                                                                              Indels
                                                                                                                                                                 0; Gaps
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EMBL; X91233; CAA62616.1; -. EMBL; X94223; CAA63914.1; -. EMBL; X94222; CAA63913.1; -. EMBL; AF031167; AAB97518.1; -.

EMBL; Y09908; CAA71044.1; -. EMBL; Z38000; CAA86100.1; -.

HGNC:5977; IL15.

MIM;

600554

PF02372; IL15;

IPR003443; Interleukin_15.

Glycoprotein; Signal; Alternative splicing.

CHAIN PROPEP cytokine; InterPro;

1 30 49 83 90 127

POTENTIAL. POTENTIAL INTERLEUKIN-15. POTENTIAL.

.) (POTENTIAL)

EMBL;

U14407; AAA21551.1; --

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SIMILARITY: BELONGS TO THE IL-15 FAMILY.
SIMILARITY: BELONGS TO THE IL-15 FAMILY.
DATABASE: NAME-R&D Systems' cytokine source book: IL15;
DATABASE: NAME-R&D Systems com/asp/g_sitebuilder.asp?bodyId=209".
WWW-"http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=209".

RESULT

Дb 20 В

Qy Дb Ωy

61 61

EDLIQSMHIDATLYTESDVHPSCKYTANKCFLLELQVISLESGDASIHDTVENLIILANN 120

SQ

SEQUENCE CONFLICT

141 162 AA;

141 18086 MW; 98.6%; 98.8%;

E -> K (IN REF.

OCE0520C1D8379E2 CRC64;

ISOFORM 3).

GLPKTE -> MDFQVQIFSFLLISASVIMSR (IN MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSA MVLGTIDLCS (IN ISOFORM IL15-S21AA) MRISKPHLRSISIOCYLCLLINSHFLTEAGIHVFILG ->

VARSPLIC VARSPLIC CARBOHYD DISULFID DISULFID

Query Match

Matches

160;

Conservative

0;

Mismatches

Score 823; DB 1; Pred. No. 2.1e-67;

Length 162;

Indels

0; Gaps

0;

0

Similarity

1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60

MRISKPHLRSISIOCYLCLLLNSHFLTEAGIHVEILGCESAGLPKTEANWVNVISDLKKI 60 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120

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Qy
                                                   IL15_FELCA
                                                                RESULT 4
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                                                                                                                                                                                                   Qγ
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30-MAY-2000 (Rel. 39, Created)
                        097687
                                  IL15_FELCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                              121 ILSSNGNITESGCKECEELEEKNIKEFLQSFVHIVOMFINTS 162
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                          121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytokine; Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                               PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAMMA BUT NOT IL-2R ALPHA
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grabstein K.H., Eisenman J., Shanebeck K., Rauch C., Srinivasan S., Fung V., Beers C., Richardson J., Schoenborn M.A., Ahdieh M., Johnson L., Alderson M.R., Watson J.D., Anderson D.M.,
                                                                                                                                                                        61
                                                                                                                                                                                61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 264:965-968(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the interleukin-2 receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning of a T cell growth factor that interacts with the beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94233380; PubMed=8178155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 49-81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Interleukin-15 precursor (IL-15).
                                                                                                                                                                                                              1 MRISKPHERSISIOCYLCLLLKSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                          1 MRISKPHERSISIOCYLCLLLNSHELTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecinae; Cercopithecus
                                                                                                                                                                                                                                                                                                        rocar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P40221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IL15_CERAE
                                                                                                                                                    EDLIQSMHIDATLYTESDVHPSCKVTANKCFLLELQVISHESGDTDIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15 WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-1
                                                                                                                                                                                                                                                                                       154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pro; IPR003443; Interleukin_15.
PF02372; IL15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U03099; AAA18416.1;
                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                   162 AA;
                                                                                                                                                                                                                                                                                                                                                                30
49
83
90
127
                                                                                                                                                                                                                                                                                     Conservative
                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                            18222 MW;
                                                                                                                                                                                                                                                                                                   95.2%;
95.1%;
                                                                                                                                                                                                                                                                               1; Mismatches
                            PRT;
                                                                                                                                                                                                                                                                                            Score 795; DB 1;
Pred. No. 6.9e-65;
                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                        INTERLEUKIN-15
                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                          1BF9A82644E1C9B7 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                             7; Indels
                                                                                                                                                                                                                                                                                                        Length 162;
                                                                                                                                                                                                                                                                                                                                                   .) (POTENTIAL).
                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                              Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
SEQUENCE FROM N.A.
                           NCBI_TaxID=9823;
                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                     Sus scrofa (Pig)
                                                                                               Interleukin-15 precursor (IL-15)
                                                                                                                                                                Q95253;
                                                                                                                                                                             IL15_PIG
                                                                                                                                                                                                                                         121 GLSSNRNITETGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                     121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003443; Interleukin_15.
Pfam; PF02372; IL15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytokine; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Lymph node;
Barger A.B., Dean G.A., Lavoy A.S.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF108148; AAD05268.1;
                                                                                                                                                                                                                                                                                                                61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Felis silvestris catus (Cat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                       1 MRILKPYLRSTSIQCYLCLLLNSHFLTEACIPVFILSCINAGLPKTEANWQDVISDLKII 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                 1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interleukin-15 precursor (IL-15)
                                                                                                                                                                                                                                                                                              DKIIQSLHIDATLYTESDVHPNCKVTAMKCFLLELHVISLESKNETIHQTVENIIILANS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15 WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30
49
83
90
                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18412 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                     81.4%; Score 680;
81.5%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                      13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
D8C7CEF7F40110DD CRC64;
                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERLEUKIN-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                     162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                        .6e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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Canals A., Grimm D.R., Gasbarre L.C., Lunney J.K., Zarlenga D.S.; "Molecular cloning of cDNA encoding porcine interleukin-15."; Gene 195:337-339(1997).

© 195:33/-339(1997).
FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF IL-15
LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).

TISSUE-Blood;

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29
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  THE COLOR OF THE PROPERTY OF OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics and the EMBL outstation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytokine; Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U42433; AAA85130.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9XSJ6;
                                                                                                  Circulating in efferent lymph.";

J. Interferon Cytokine Res. 0:0-0(1999).

J. Interferon Cytokine Res. 0:0-0(1999).

J. Interferon Cytokine ThAT STIMULATES THE PROLIFERATION OF T.

LYMPHOCYTES. STIMULATED BY IL-15 REQUIRES INTERACTION OF IL-15 LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-2R AITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ovis aries (Sheep).
                                                                                                                                                                                                                                                                 Casey G.J., Chaplin P.J.: "Isolation of interleukin-15 meNA transcripts from T and B cells "Isolation of interleukin-15 meNA transcripts from T and B cells
                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interleukin-15 precursor (IL-15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 NLSSIENKTELGCKECEELEEKSIKEFLKSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 SLSSNGNVTESGCKECEELEEKNIKEFLDSFVHIVDMFINTS 162
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [L15_SHEEP
                                                    -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOCGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE IL-15 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRISKPHLRSISIOCYLCLLLNSHFLTEAGIHVEILGCESAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRILKPYLRSTSIQCYLCLLLNSHFLTEAGIHVFILGCISASLPKTEANWQYVINDLKTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EHLIQSIHMDATLYTESDAHPNCKVTAMQCFLLELRVILHESKNATIYEIIENLTMLANS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDLIOSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF02372; IL15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR003443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18554 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.2%; Score 645; DB 1; 77.8%; Pred. No. 2.2e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interleukin_15.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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the European Bioinformatics Institute.

the Swiss Institute of Bioinformatics and the EMBL outstation

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RESULT 8
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                            Anderson D.M., Johnson L., Glaccum M.B., Copeland N.G., Gilbert D.J., Jenkins N.A., Valentine V., Kirstein M.N., Shapiro D.N., Morris S.W., Grabstein K., Cosman D., "Chromosomal assignment and genomic structure of IL15."; Genomics 25:701-706(1995).

Genomics 25:701-706(1995).

THAT STIMULATES THE PROLIFERATION OF TLYMPHOCYTES. STIMULATES THE PROLIFERATION OF IL-15 LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION BY IL-15 LYMPHOCYTES. STIMULATION BY IL-15 LYMPHOCYTES.
                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=WC/REJ X C57BL/6J: TISSUE=Bone marrow;
MEDLINE=95278940; PubMed=7759105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interleukin-15 precursor (IL-15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IL15_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 EDLIQSMHIDATLYTESDYHPSCKYTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                  SIMILARITY: BELONGS TO THE IL-15 FAMILY.
                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                         WITH COMPONENTS OF IL-2R,
GAMMA BUT NOT IL-2R ALPHA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF02372; IL15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi;
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77.2%;
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                                                                                                                                                                                                                                            INCLUDING IL-2R BETA AND PROBABLY IL-2R
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                    Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                      STRAIN=Wistar; TISSUE=Spleen;
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        STRAIN=Sprague-Dawley; TISSUE=Jejunum; MEDLINE=97098212; PubMed=8942753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P97604; O54847;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                    Reinecker H.C., Macdermott R.P., Mirau S., Dignass A., Podolsky D.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAT
                                                                                                                                                                                                                                                                                   Gastroenterology 111:1706-1713(1996).
                                                                                                                                                                                                                                                                                                        "Intestinal epithelial cells both express and respond to
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (LONG FORM)
                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interleukin-15 precursor (IL-15).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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Pfam; PF02372; IL15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:103014;
                                                                                                           SIMILARITY: BELONGS TO THE IL-15 FAMILY.
                                                                                                                              SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKILKPYMRNTSISCYLCFLLNSHFLTEAGIHVFILGCVSVGLPKTEANWIDVRYDLEKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESLIQSIHIDTTLYTDSDFHPSCKVTAMNCFLLELQVILHEYSNMTLNETVRNVLYLANS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
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49
83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                     (LONG AND SHORT FORMS).
                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.8%;
71.6%;
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nucleoside transporter FUN26.
                                                                                                                                                                                                                          STRAIN=S288c / AB972;
MEDLINE=93209532; PubMed=8458570;
Quellette B.F.F., Clark M.W., Keng T., Storms R.K., Zhong W.W.,
Zeng B., Fortin W., Delaney S., Barton A.B., Kaback D.B., Bussey H.;
Zeng B., Fortin W., Delaney S., Barton A.B., Kaback D.B., Bussey H.;
Sequencing of chromosome I from Saccharomyces cerevisiae: analysis
"Sequencing of chromosome I from Saccharomyces cerevisiae: analysis
of a 32 kb region between the LTE1 and SPO7 genes.";
                          Vickers M.F., Yao S.Y., Baldwin S.A., Young J.D., Cass C.E.;
"Nucleoside transporter proteins of Saccharomyces cerevisiae.
"Nucleoside transporter proteins of Saccharomyces cerevisiae.
Demonstration of a transporter (FUI1) with high uridine selectivity
Demonstration of a transporter (FUN26) with broad nucleoside
in plasma membranes and a transporter (FUN26) with broad nucleoside
selectivity in intracellular membranes.";
J. Biol. Chem. 275:25931-25938(2000).
J. BIOL. Chem. 275:25931-25938(2000).
J. BIOL TO TRANSPORT NUCLEOSIDES
CYTIDINE) AND MOST LIKELY FUNCTIONS TO TRANSPORT NUCLEOSIDES
CYTIDINE) AND MOST LIKELY FUNCTIONS
                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TLSSNKNVIESGCKECEELEERNFTEFLQSFIHTVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4932;
                                                                                                                                                            MEDLINE=20408929; PubMed=10827169;
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                              CHARACTERIZATION.
                                                                                                                                                                                                              Genome 36:32-42(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESLIQFIHIDTTLYTDSDFHPSCKVTAMNCFLLELQVILHEYSNMTLNETVRNVLYLÄNS 120
SUBCELLULAR LOCATION: Integral membrane protein (Potential)
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               ACROSS INTRACELLULAR MEMBRANES
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108
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71.0%;
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MISSING (IN SHORT ISOFORM)
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pred. No. 5.9e-48;
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(POTENTIAL).
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ALD PRICE REPORT OF THE PR
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TRZA_RHOCO
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Q52725;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
5-triazine hydrolase (EC 3.8.1.-) (N-ethylammeline chlorohydrolase).
                                                                                                  "Cloning and expression of the s-triazine hydrolase gene (trzA) from Promosococcus corallinus and development of Rhodococcus recombinant Rhodococcus corallinus and development of Rhodococcus recombinant strains capable of dealkylating and dechlorinating the herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 YLVLSIFTTEVVTLVFPVFASATYVTGLPLSNAQYIPLIFTLMNLGDLYGRVIADWPMFR 402
                            J. Bacteriol. 177:5748-5755(1995)
                                                                                                                                                                               Shao Z.Q., Seffens W., Mulbry W., Behki R.M.;
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                    Actinomycetales; Corynebacterineae; Gordoniaceae; Gordonia.
                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteria (class);
                                                                                                                                                                                                                                                                                                                                                                                       Rhodococcus corallinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           461
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                                                                                                                                                                                                              MEDLINE=96011356; PubMed=7592318;
                                                                                                                                                                                                                                       STRAIN=NRRL 15444R;
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=36822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 YLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKIEDLIOSMHIDATLYT 75
                                                                            atrazine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 ESDVHPS-----CKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS----- 123
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                         FUNCTION: HYDROLYTIC DEAMINATION OF THE S-TRIAZINE SUBSTRATE
        MELAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40;
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39; 2a57; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43C92A3E9A3D8D50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          476 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usage
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RESULT 12
REB1_KLUL#
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                    EMBL; L03789; AAA61343.1; --
PIR; A48077; A48077
HSSP; P06876; 1MBC
Pfam; PF00249; myb_DNA-binding; 3
                                      TRANSFAC; T01245;
                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation -
                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                         Morrow B.E., Ju Q., Warner J.R.; "A bipartite DNA-binding domain in yeast Reblp."; Mol. Cell. Biol. 13:1173-1182(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=93140755; PubMed=8423784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kluyveromyces lactis (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REB1_KLULA
Q05950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-binding protein REB1 (QBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L16534; AAA90931.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: Melamine degradation pathway; first step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380 IGSLEAGKRADIITLDLRHAQTTPAHDLAATIVFQAYGNEVNDVLVNGSV 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 TVGIGTDDANCNDSVNLISDMKVLALIHRAAHRDASIITPEKIIEMATIDGARCIGMADQ 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 VISLESGDAS------IHDTVENLIILAN----NSLSSNGNV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 SAGLPKTEANW----VNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCELLELQ 96
                                                                                                                                                                                                                                                                                           THE ENHANCER AND THE PROMOTER OF RNA TRANSCRIPTION, AS WELL AS UPSTREAM OF MANY GENES TRANSCRIBED BY RNA POLYMERASE II. IT IS ESSENTIAL FOR CELL GROWTH, MAY STUMULATE OR INHIBIT TRANSCRIPTION. SPECIFICALLY RECOGNIZE THE SEQUENCE 5'-CCGGGTA-3' OR 5'-CGGGTRR-3' (WHERE R IS ANY BURINE) (BY SIMILARITY).
                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: DNA-BINDING PROTEIN THAT RECOGNIZES SITES WITHIN BOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF01685; ATZ_TRZ; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 9.9%; Score 82.5; Di Similarity 23.6%; Pred. No. 3.9;
               IPR001005; Myb_DNA_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 AA; 50727 MW; 64D953DB2E92C73E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002604; ATZ_TRZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    595 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage by
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DR DR DR KW
 Best Local Similarity
                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                             SEQUENCE
                                                                                    Pfam: PF00290; trp_syntA; 1.
ProDom: PD001535; Trp_synthaseA; 1.
TICREAMS: TICR00262: trpA; 1.
PROSITE; PS00167; TRP_SYNTHASE_ALPHA; 1.
                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHATE.

-!- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate - L-tryptophan + glyceraldehyde 3-phosphate + H(2)0.

-!- PATHMAY: Tryptophan biosynthesis; fifth (last) step.

-!- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS (BY
                                                                      Tryptophan biosynthesis; Lyase.
                                                                                                                                                                                                       EMBL; U09185; AAA92797.1; - HSSP; P00929; 2WSY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insect Mol. Biol. 4:47:59(1995).
-!- FUNCTION: THE ALPHA SUBUNIT IS RESPONSIBLE FOR THE ALDOL CLEAVAGE OF INDOLEGLYCEROL PHOSPHATE TO INDOLE AND GLYCERALDEHYDE 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        044604;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                               InterPro; IPR003009; FMN_enzyme.
InterPro; IPR002028; Trp_synthaseA.
                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE TRPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endosymbiont (Buchnera)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genetics of the tryptophan biosynthetic pathway of the prokaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95261545; PubMed=7742976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buchnera aphidicola (subsp. Schlechtendalia chinensis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tryptophan synthase alpha chain (EC 4.2.1.20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=118110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRPA_BUCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00395; SANT; 4.
PROSITE; PS00037; MYB_1; 2.
PROSITE; PS00334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear protein; DNA-binding; Transcription regulation; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 NDDQQDDVSNLIQEAAAKASHIINPATQSNGKSFDESEEEALEQFIKEYQKI 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 DASIHDTVENLIILANNSLSSNGN-VTESGCKECEELEEKNIKEFLDSFVHI 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 PKKEKSEERSYGDLSNIDDHVDDVSVSGSIPSQVRLKKTAEVLP------KVLSSESH 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 PKTEANWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y., Baumann P., Moran N.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
                                                     269 AA; 30301 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         595 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.8%; Score 81.5;
25.0%; Pred. No. 6.
                   9.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the aphid Schlechtendalia chinensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
Score 81; DB
Pred. No. 2.7;
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                                                   7879A03A5C7A50AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYB 1
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               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 595;
             Length 269;
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25.5%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kawanomoto M., Motojima K., Sasaki M., Hattori H., Goto S.; "CDNA cloning and sequence of rat ribonuclease inhibitor, and tissue distribution of the mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-1992 (Rel. 24, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RINI_RAT
                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribonuclease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 STGYIYLLS-RSGVTGTDKKIIVPSLNLIKNLKKITE 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 DSVLIADLPVEESN-----DFRKCAIANNISSVFVCP-----HDAKKNVIKKISLY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- TISSUE SPECIFICITY: BRAIN, HEART, LUNG, LIVER, SPLEE.
KIDNEY; HIGHEST IN THE LUNG AND LOWEST IN THE HEART.
-i- SIMILARTIY: CONTAINS 15 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION IN THE MODULATION OF CELLULAR ACTIVITIES.
-!- SUBJUNT: FORMS A TIGHT ONE-TO-ONE COMPLEX WITH THE RNASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92162755; PubMed=1536887;
                                                                                                                                                                            SMART; SM00370; LRR; 12.
SMART; SM00368; LRR_RI; 1
                                                                                                                                                                                                                                                                                              EMBL; X62528; CAA44388.1; ~.
                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION:
                                                                                                                                                                                                          Pfam; PF00560; LRR; 3.
                                                                                                                                                                                                                                                                   HSSP; P10775;
                                                                         REPEAT
                                                                                       REPEAT
                                                                                                     REPEAT
                                                                                                                  REPEAT
                                                                                                                                  REPEAT
                                                                                                                                                             Repeat;
                                                                                                                                                                                                                       InterPro; IPR003592; LRR_out
                                                                                                                                                                                                                                     InterPro; IPR003590; LRR_RNinh
                                                                                                                                                                                                                                                     InterPro; IPR001611; LRR.
                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 IQKAHLRAFSSKMNIYLCFEMLQKIRKKYNTIPIGLLLYANLIFKFGINNFYLKCFNVGI 123
              REPEAT
                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISKPHLRSIS--IQCYLC--------LLLNSHFLTEAGIHVFILGCFSAG- 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------LPKTEANWVNVISDLKK--IEDLIOSMHIDATLYTESDVHPSCKVTAMKCFLL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELQVISLESGDASIHDTVENLIILANNSLSSNGNVTE 130
                                                                                                                                                                                                                                                                              s20597; s20597.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40; Conservative
                                                                                                                                                             Leucine-rich repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biophys. Acta 1129:335-338(1992).
TION: INHIBITOR OF PANCREATIC RNASE AND ANGLOGENIN. MAY
 44
72
101
129
158
158
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215
243
272
                                                                                                                                                                                                                                                                   2BNH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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157
185
214
214
271
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299
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   LRR A1.
LRR B1.
LRR A2.
LRR A3.
LRR B3.
LRR B3.
LRR A4.
LRR B4.
LRR B5.
LRR B5.
LRR B5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEART, LUNG, LIVER, SPLEEN, TESTES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      456 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Gaps
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HCYG_SEPOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-Jun-2002 (Rel. 41, Last annotation update)
Haemocyanin, units G and H (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Sepioida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sepia officinalis (Common cuttlefish)
                                                                                                                                                                                                            "Evidence for a cysteine-histidine thioether bridge in functional units of molluscan haemocyanins and location of the disulfide bridges in functional units d and g of the beta-c-haemocyanin of Helix
                                                                                                                                                                                                                                                                                                                                                                                                          Sepia officinalis and partial amino-acid sequence of functional
                                                                                                                                                                                                                                                                                                                                                                                                                             PARTIAL SEQUENCE (H SUBUNIT).
Vanderzande M., Gielens C., Preaux G.,
"Isolation of functional units g and h from the haemocyanin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           via cDNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Declercq L., Witters k., Freaux 6.; "Partial sequence determination of Sepia officinalis haemocyanin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 20-436 AND 446-560 FROM N.A. Declercq L., Witters R., Preaux G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6610;
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                                                                                                                                                                                                                                                                             Gielens C., de Geest N., Xin X.-Q., Devreese B., van Beeumen J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 CKDLCDVVASKASLQELDLGSNKLGNTGTAALCSGL-LLPSCRLRTLWLWDCDVTAEGCK 269
Interpro; IPR002227; Tyrosinase.
prINTS; PR00092; TYROSINASE.
pROSITE; PS00497; TYROSINASE_1; 1.
                                                              -i- SUBUNIT: DECAMERS OF LARGE IDENTICAL SUBUNITS (390 kDa), CONTAINING 8 GLOBULAR OXYGEN-BINDING FUNCTIONAL UNITS.
-i- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
                                                                                                                                                                                                                                                                 Preaux G.;
                                                                                                                                                                                                                                                                                               MEDLINE=98000289; PubMed=9342242;
                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-19 AND 230-249, AND THIOETHER BOND.
                                                                                                                                                                                                                                                                                                                                                            Invertebrate Dioxygen Carriers, pp.125-129, Leuven University Press,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leuven (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Invertebrate Dioxygen Carriers, pp.131-134, Leuven University Press,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 DLCRVLRAKQSLKE 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 E-CEELEEK-NIKE 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 LVLSNNDFHEAGIHTLCQG------
                                                                                                                                                 Eur. J. Biochem. 248:879-888(1997).
-i- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS
-i- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS
OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                                                                                                                               Leuven (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (In) Preaux G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 LLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKIEDLIQSMHIDATLYTESD 78
                                                                                                               -!- COFACTOR: CONTAINS TWO COPPER ATOMS PER FUNCTIONAL UNIT.
                                                                                                                                                                                                 pomatia.",
                                                                                                                                                                                                                                                                                                                                                                                   (In) Preaux G., Lontie R. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 VHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSS----NGNVTESGCK 134
                                                 SUBFAMILY
                                                                                                                                 ARTHROPODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
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385
413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRR B6.
LRR A7.
LRR B7.
LRR A8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
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Search completed: February 20, 2003, 16:29:04 Job time : 18.5 secs
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9.5%; Score 79; DB 1; Length 560;
Best Local Similarity 25.0%; Pred. No. 9.7;
Matches 38; Conservative 23; Mismatches 53; Indels 38; Gaps
                                      194 KNVNSLSPS------EIKNLRDAL 211
                                                            117 LANNSLSSNGNVTESGCKECEELEEKNIKEFL 148
                                                                         135 PMEALFENDSKIHLEVEIQSVDGAILDSHSLPTPSLIYAPAKGLVSQHIEDHDT-ETLIR 193
                                                                                                                                                                                                                                                                          METAL
DISULFID
                                                                                                                                                                                                                                 SEQUENCE
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METAL
METAL
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THIOETH
                                                                                     70 --DATLYTESDVHPSCKVTAMKCELLELQVI------SLESGDASIHDTVENLII 116
                                                                                                                   85 SADVHLKVCNAADCH---EAGV-VEVLGA-----RTEMPWHFDRNYKMDITDVLHEMHI 134
                                                                                                                                 10 SISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKIEDLIQSMHI 69
                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
THIOETH
                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00498; TYROSINASE_2; 1.
Oxygen transport; Transport; Copper; Hemolymph;
                                                                                                                                                                                                                                                                                                                                                                             METAL
                                                                                                                                                                                                                                                                                                                                                                                                   NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Repeat.
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236
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240 N-LINKED (GLCNAC. . .) (POTENTIAL).
63362 MW: BD966BE34307B387 CRC64;
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COPPER A (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

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UNIT H.
BY SIMILARITY.
BY SIMILARITY.
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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9.4	9.4	9.4	9.5	9.5	9.5	9.6	9.6	9.6	9.6	9.6	9.7	9.8	9.8	9.8	9.8	9.8	. 8		9.8	9.9	9.9	10.1	10.1	10.1	10.1	10.2	10.2
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Q97MN8 097258	065990	Q9FY96	09A.TA7	061493	Q9K828)9ZSX2	OBRCX4	09M078	016199	0901V4	0900Z4	09IK12	Q91K13	Q91K14	21687	Q95JZ9	Q71154	Q8YYY2	Q8VY37	085479	OBREU9	Q9T0B6	Q8VY35	Q9PIB4	046295)37631	002497
	O65990 clostridium	09file Shewanella	Obi493 drosophila	Variation Decitions ha	Ograsa zea mays (m	Q8rcx4 thermoanaer	Q9m0/8 arabidopsis		09u1v4 caenorhabdi		human	namur	numan	caenorh	031687 i ii			zed mays	zea mays		_	OG+Obe see mays (m	OBVINGE COMPYLOBACE	crostridium)

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OBSPYO;
OBSPYO;
O1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Interleukin 15 (Fragment).
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Xiang Z., Byrne K.M., Michal J.;
"Cytokine expression in muscle satcllite cells of canine.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF479882; AAL87133.1;
NON_TER 128 128
121 DLSSKGNI 128
                                    121 SLSSNGNV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O8SPY0
                                                      61 DNLIQCIHMDTTLYTESDYHPSCKITAMKCFLLELGVISLESGSHPIKEAVENLIILANS 120
                                                                            61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                128 AA; 14192 MW; FC6BC2C2E1765934 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                    63.8%; Score 533; DB 6; Length 128; 79.7%; Pred. No. 4e-45; ative 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                    0; Gaps
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Q9DEV5
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                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9W756
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9DBV5;

01-MAR-2001 (TrEMBLrel. 16, Created)

01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

Interleukin 15.
Best Local Similarity
              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9DEV5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stepaniak J.A., Kolodsick J.E., Hu W., Sundick R.S.; "Chicken interleukin 15 precursor, allelic variant."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AY005476; AAG02253.1; "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pfam; pF02372; IL15
SEQUENCE 187 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
Interleukin-15 precursor (Interleukin 15 precursor).
                                                                                                                                                                                                                                                                                                                                                                                                                     Q9W756;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9W756
                                                                                                                                                                                                                                                                                                            Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken)
                                                                                  Choi K.D., Lillehoj H.S., Burnside J.;
"Gallus gallus mRNA for IL-15 precursor.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF152927; AAD38392.1;
EMBL, AF153997; AAF6446.1;
EMBL, AF139997; AAF6446.1;
                                                                                                                                                                                                                                   STRAIN-SCWL; TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 LIILANNSLSSNGN-------VTESGCKECEELEEKNIKEFLDSFVHIV 155
                                                                                                                                                                                                         Burnside J., Sofer L.; submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                 STRAIN=SC;
                                             SEQUENCE
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 ELIK---TSEDIDVSLYTANTYEDIECQEPVMRCFFLEMKVILHECGIKKCSRKHD-VWN 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 KTHVKSICLQYQLYLLLNSHFFCLLKNKTGLTIFFL---CAYVPKTEANHCKWSDVLKDL 78
                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 KPHLRSISIQCYLCLLLNSHFL----TEAGIHVFILGCFSAGLPKTEAN---WVNVISDL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IL-----KNGNARFATYOLNSTTSKKCKECEEYEEKNFTEFIQSFVKVI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKIEDLIQSMHIDATLYTESDVHP-SCKVTAMKCFLLELQVISLESGDASI---HDTVEN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67;
                                          PF02372; IL15;
NCE 187 AA; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR003443; Interleukin_15.
2372; IL15; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                          IPR003443; Interleukin_15
                                                                                                                                                                 TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21879 MW; B701CFCC7431B658 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.6%; Score 247; DB 13; 39.0%; Pred. No. 1.3e-16; tive 22; Mismatches 47
                                                21964 MW; 470601EBF8837095 CRC64;
    28.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
    Pred. No. 1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                     Score 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 47; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                           187 AA
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                     DB 13; Length 187;
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                                                                                                                                                          073883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-KESTREL LEGHORN: TISSUE-SPLEEN;
Hutchins J.E., Tyczkowski J.K., Poston R.M., Hester J.B.,
Girardi R.S., Liu H., Doelling V.W., Ricks C.A., Bland M.M.;
"Gallus gallus mrNA for IL-2 precursor.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF033563; AAB87502.1:
Interpro; IPR003743; Interleukin-2.
Interpro; IPR003443; Interleukin-15.
Pfam; PF02372; ILI5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           042288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euceleus Comil, Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 -----RNIWKNGNARFATYQLNSTTAKKCKECEEYEEKNFTEFIQSFVKVI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interleukin-2 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 NLIILANNSLSSNGN------VTESGCKECEELEEKNIKEFLDSFVHIV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00189; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 ELIK---TSEDIDVSLYTANTYEDIECQEPVMRCFFLEMKVI-LHECDIKKCSRKHDV-- 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 KKIEDLIQSMHIDATLYTESDVHP-SCKVTAMKCFLLELQVISLESGD----ASIHDTVE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 KTHYKSICLQYQLYLLLNSHFFCLLKNKTGLTIFFL---CAYVPKTEANHCKWSDVLKDL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
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                                                                                                       073883;
                                                                                                                               073883
                                                                                                                                                                                                                                                                                         118 ICEANNKKKFPDFLHELTNFV 138
                                                                                                                                                                                                                                                                                                                                                       135 ECEELEEKNIKEFLDSFVHIV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 VETLGCESAGLPKTEA------NW---VNVISDLKKIEDLIQSMHIDATLYTESDVHP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 SCKVTAMKCFLLELQVISLESGDASIHDT-VENLIILANNSLSSN------GNVTESGCK 134
                                                                                                                                                                                                                                                                                                                                                                                                              62 ECTQQTLQCYLGEVVTLKKETED----DTEIKEEFVTAIQNIEKNLKSLTGLNHTGSECK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 VLIFGCISVAMLMTTAYGASLSSEKWKTLQTLIKDLEILENIKNKIHLE--LYTPTETQ- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 AA;
                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16429 MW;
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30
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26.2%; Pred. No. 0.0013;
Live 25; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7DCDFEACBD48F5AC CRC64;
                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13; Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Indels 25; Gaps
                        update)
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RESULT 6
Q9PT81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
proliferation assays despite limited amino acid sequence identity.";
                MEDLINE=20177011: PubMed=10714551;
Lawson S.A., Rothwell L., Kaiser P.;
"Turkey and chicken interleukin-2 cross-react in in vitro
                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                     Meleagris gallopavo (Common turkey).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                     SEQUENCE FROM N.A.
                                                                                                       Archosauria; Ayes; Neognathae; Galliformes; Meleagrididae; Meleagris
                                                                                                                                                                                                                                                              Q9PT81
                                                                                                    NCBI_TaxID=9103;
                                                                                                                                                                           Interleukin-2 precursor.
                                                                                                                                                                                                                                               Q9PT81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Choi K.D., Lillehoj H.S., Song K.D., Han J.Y.; "Molecular and Functional Studies of Chicken IL-15 which Promotes the Growth of gamma/delta TCR T Lymphocytes: Phenotypic and Functional Characterization of IL-15 dependent gamma/delta T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00189; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: AP017645; AAC96064.1; -.
EMBL: AV029588; AAK37775.1; -.
InterPro: IPR000779; Interleukin-2.
InterPro: IPR003443; Interleukin_15.
Pfam: PP02372; IL15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yu L., Li J.R., Huang Y.W., Meng S.S.; "Cloning and sequence analysis of a Chinese local chicken IL-2 gene."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ224516; CAA12025.1; -.
                                                                                                                                                                                                                                                                                                                                      118 ICEANNKKKFPDFLHELTNFV 138
                                                                                                                                                                                                                                                                                                                                                                 135 ECEELEEKNIKEFLDSFVHIV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERLEUKIN-2 OR IL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IL-2 precursor (Interleukin-2).
                                                                                                                                                                                                                                                                                                                                                                                            62 ECTQQTLQCYLGEVVTLKKETED----DTEIKEEFVTAIQNIEKNLKSLTGLNHTGSECK 117
                                                                                                                                                                                                                                                                                                                                                                                                                       82 SCKVTAMKCFLLELQVISLESGDASTHDT-VENLIILANNSLSSN-----GNVTESGCK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 VFILGCESAGLPKTEANWVN------VISDLKKIEDLIQSMHIDATLYTESDVHP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 VLIFGCISVAMLMTTAYGASLSSAKRKPLQTLIKDLEILENIKNKIHLE--LYTPTETQ- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 AA;
                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mariani P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.5%; Score 112.5; DB 13; Length 143; 25.5%; Pred. No. 0.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16337 MW; B1BCFEA97A54846F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERLEUKIN-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                       143 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25; Gaps
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042396
            RESULT 8
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                                                                                                                                Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db
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                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF209705; AAF33206.1; ... InterPro: IPR000779; Interleukin-2. InterPro: IPR003443; Interleukin_15.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02372; IL15; SMART; SM00189; IL2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last seq.
01-JUN-2001 (TrEMBLrel. 17, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meleagris gallopavo (Common turkey).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                            122 NDKKNFPDFLQQLTNLL 138
                                                                                            139 LEEKNIKEFLDSFVHIV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Turkey interleukin-2 gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Romero C.H., Cai X.Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interleukin-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9IAC7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9TAC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000779; Interleukin-2.
InterPro; IPR003443; Interleukin_15.
Pfam; PF02372; IL15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Interferon Cytokine Res. 20:161-170(2000). EMBL; AJ007463; CAB65230.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00189; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                       62 ECSQQTLQCYLEEMVMLKKEIEDEPEIKNEFKNALQNIKKNLHRLKDLSPTGGECKICEA 121
                                                                                                                                                     82 SCKVTAMKCFLLELQVISLESGD-ASIHDTVENLIILANNSLSSNGNVTESG--CKECEE 138
                                                                                                                                                                                                                         33 VFILGCFSAGLPKTEANWVN------VISDLKKIEDLIQSMHIDATLYTESDVHP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 NDKKNFPDFLQQLTNFV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 LEEKNIKEFLDSFVHIV 155
                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                        5 VLIFSCISVALLMTTAYGASLSPEKLEILPALIKDLEILEESKNKIHV--VLYTPNEI-K 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 ECSQQTLQCYLEEMVMLKKEIEDEPEIKNEFKNALQNIKKNLHRLKDLSPTGGECKICEA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 VFILGCFSAGLPKTEANWVN------VISDLKKIEDLIQSMHIDATLYTESDVHP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 VLIFSCISVALLMTTAYGASLSPEKLEILPALIKDLEILEESKNKIHV--VLYTPNEI-K 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCKVTAMKCFLLELQVISLESGD-ASIHDTVENLIILANNSLSSNGNVTESG--CKECEE 138
                                                                                                                                                                                                                                                                 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34;
                                                                                                                                                                                                                                                                                                                              143 AA; 16442 MW; 1A4AD959348BB22B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 AA;
                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aves; Neognathae; Galliformes; Meleagrididae; Meleagris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                            13.2%; Score 110.5;
24.1%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16511 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.4%; Score 111.5; DB 24.8%; Pred. No. 0.0025;
                                                                                                                                                                                                                                                            30; Mismatches 57; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERLEUKIN-2
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                                                                                                                                                                                                                                                                                No. 0.0031
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                                                                                                                                                                                                                                                                                             DB 13; Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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AC ID

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PRELIMINARY;

PRT;

143 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                           Matches
                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Interleukin-2 (Fragment).
Meleagris gallopavo (Common turkey).
Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02372; IL15; SMART; SM00189; IL2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003443; Interleukin_15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sundick R.S., Gill-Dixon C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=OBESE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A cloned chicken lymphokine homologous to both mammalian IL-2 and IL-
                                                                                                                                                 InterPro; IPR000779; Interleukin-2.
InterPro; IPR003443; Interleukin_15
Pfam; PF02372; IL15; 1.
                                                                                                                                                                                              Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF308569; AAG35189.1; -
                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                            Q9DDN9;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9DDN9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000779; Interleukin-2
                                                                                                                                    SMART; SM00189; IL2;
                                                                                                                                                                                                                              "Turkey interleukin-2.";
                                                                                                                                                                                                                                             Hu W., Kolodsick J.E., Stepaniak J.A., Sundick R.S.;
                                                                                                                                                                                                                                                            TISSUE=SPLEEN;
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9103;
                                                                                                                                                                                                                                                                                                                         Archosauria;
                                                                                                      SEQUENCE
                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 ICEANNKKKFPDFLHELTNEV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 ECEELEEKNIKEFLDSFVHIV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 ECTQQTLQCYLGEVVTLKKETED----DTEIKEEFVTAIQNIEKNLKSLTGLNHTGSECK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 SCKYTAMKCFLLELQVISLESGDASIHDT-VENLIILANNSLSSN------GNVTESGCK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 VFILGCFSAGLPKTEANWVN------VISDLKKIEDLIQSMHIDATLYTESDVHP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 VLIFGCISVATLMTTAYGASLSSAKRKPLQTLIKDLEILENIKNKIHLE--LYTPTETQ- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
           38 CFSAGLPKTEANWVN------VISDLKKIEDLIQSMHIDATLYTESDVHPSCKVT 86
                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunol. 0:0-0(1997)
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                                           31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 AA;
                                                                                                      135 AA; 15460 MW; 326F88A3563D13E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                           Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                       Aves; Neognathae; Galliformes; Meleagrididae; Meleagris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IL2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16307 MW;
                                                          12.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.1%;
25.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 109.5; DB Pred. No. 0.004;
                                                                        Score 101.5;
                                                           Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               135 AA.
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                                                                          DB 13;
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                                           55; Indels
···
                                                                          Length 135;
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                                                                                                                                                                                                                                                                 RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              092GE7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein RC1176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q92GE7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-MALISH 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 293:2093-2098(2001).
EMBL; AE008665; AAL03714.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Samson D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21442074; PubMed=11557893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rickettsiaceae; Rickettsieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsia conorii
                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Interleukin 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Raoult D.
                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                              Q9нвЕ4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 FPDFLQQLTNLL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 IKEFLDSFVHIV 155
                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                          Q9HBE4;
SEQUENCE FROM N.A.
                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                       175 PRESFINT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 TLQCYLEEMVMLEKEIEDEPEIKNEFKNALQNIKKNLHRLKGLSPTGGECKICEANDKKN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 AMKCFLLELQVISLESGD-ASIHDTVENLIILANNSLSSNGNVTESG--CKECEELEEKN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                 103 GDASIHDTVENLIILANNSLSSNGNVTES-----GCKECEELEEKNIKEFLDSFVHIV- 155
                                                                                                                                                                                                                                                                                                                                                              156 --DMFINT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 NIEQSFNESPNDFSILHQECNNGLNIPINNIFIDAENNPH-----ILLQQTVTPHQN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 SISIQCYLCLLLN------SHFLTEAGIHVF-----ILGCFSAG--LPKTEANWV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 11.7%; Score 97.5; DB 16; Length 433; Local Similarity 19.7%; Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CISVALLMTTAYGASLSPEKLEILPALIKDLEILEESKNKIHV--VLYTPNEI-KECSQQ 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 NINFKCVMPIFSNEIVSRLSGNVSH1IHKLSSTIFSSVYSTVEGAFKKGYIVDNTQCNWK 65
                                                                                                                                                                                                                                                                                                                                                                                            GTASI---LSQLYKVMNDYIFSQGNITETSGADFLGLNECTKEEAMSALQNYNAYTETLI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVISDLKKIEDLIQSMHIDA-----TLYTESDVHPSCKVTAMKCFLLELQVISLES 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  433 AA; 48342 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                              PRELIMINARY;
                                                                          Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4934702460B02EE6 CRC64;
                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     433 AA.
                                                                                                                                                                                                                                162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65; Indels 47; Gaps
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Qγ
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128 POLPMVGINTTAGTGSEMTLFAIITDEERHIKMALVDKHLTPTIAVNDPMLMLAMPKSLT 187
                               121 -SLSSNGNVTESGCKECEEL-----EEKNIKEFL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                PROSITE; PS00060; ADH_IRON_2; 1.
                                                                                                                                                                                                                                                                                PROSITE; PS00913; ADH_IRON_1; 1.
                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                 Pfam; PF00465; Fe-ADH; 1
                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL; AP003186; BAB80155.1; -.
                                                                                                                                                                                                                                                          Complete proteome
                                                       70 NPTVKNÝNDGLALLKÉKECDFÝÍSÍ--GGGŠAHDCAKGIALLÁTNGGEIKDYEGVDKSKK 127
                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                      Shimizu T.
                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=11792842;
                                                                                80 HPSCK-VTAMKCFLLELQ---VISLESGDASIHDTVENLIILANN------ 120
                                                                                                            12 LMGADCLKDÁGDQÝGELG-FKKALÍVŤD-KVLGOÍGÍVKKVTDVLDNKNÍEVALÍVDETKP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                       20 LLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKIEDLIQSMHIDATLYTESDV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium perfringens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADH OR CPE0449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alcohol dehydrogenase.
                                                                                                                                                                                         Local Similarity
les 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68NX80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68NX80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20531754; PubMed=11081504; Parrish-Novak J. Dillon S.R. Nelson A., Hammond A., Sprecher C., Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S., Conkin D., Presnell S.R., Berry J., Shiota F., Bort S., Clege C., Moore M., Grant F.J., Lofton-Day C., Glibert T., Rayond F., Ching A., Yao L., Smith D., Webster P., Whitmore T., Mudrer M., Kaushansky K., Holly R.D., Foster D., "Interleukin 21 and its receptor are involved in NK ceil expansion and Nature 408:57-63(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 TVENLII--LANNSLSSNGNVTES---GCKECEELEEKNIKEFILDSEVHIVDMFIN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 RIINVSÍKKÉKRKPPSTNAGRROKHRLTÖPSCDSVEKKPPKÉFÉLERFKSLLOKMÍH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 IDIVDQLKNYVNDLVPEF-----LPAPEDVETNCEWSAFSCF----QKAQLKSANTGNNE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 VNVISDLKK-IEDLIOSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
, Ogasawara N., Hattori M., Kuhara S., Hayashi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                            IPR001670; Fe-ADH.
                                                                                                                                                                                                                               382 AA; 40823 MW; 80300D0269F22E32 CRC64;
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       icutes; Bacillus/Clostridium group; Clostridia; Clostridiaceae; Clostridium.
                                                                                                                                                                                  11.0%; Score 92; DB 16; Length 382; 23.6%; Pred. No. 0.72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18652 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.3%;
25.0%;
                                                                                                                                                                             29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 94.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54EFD4EED3AB97FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 AA
                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 162;
                                                                                                                                                                          Indels
                                                                                                                                                                        60;
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Q9ATD8
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RP
RC
RX
RA
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RT
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288
 "Cotton seed fibers are trichomes."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF336279; AAK19612.1; HSSP; P36956; IAM9. InterPro; IPRO01092; HLH_basic. PF6am; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                                                                   STRAIN=ACALA MAXXA; TISSUE=DAY OF ANTHESIS OVULE;
                                                                                                                                                     NCBI_TaxID=3635,
                                                                                                                                                                    Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
                                                                                                                                                                                                 Gossypium hirsutum (Upland cotton)
                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                              GHDEL61
                                                                                                                                                                                                                                                                                                Q9ATD8;
                                                                                                                                                                                                                                                                                                            Q9ATD8
                                                                                                                                                                                                                                                                                                                                                                   130 MKNSHD-----EETIKSNAKIFVES 149
                                                                                                                                                                                                                                                                                                                                                                                             125 NGNVTESGCKECEELEEKNIKEFLDS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Complete SEQUENCE 167 AA; 18821 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H., "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL: AP003185; BAB79748.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium perfringens
                                                                                                                                                                                                                                                                                                                                                                                                            70 RTVSETGKLNNTMIEGLERSNNFFKCLIEDLKGVKVPEKFASYNDDIINNLNKAKTSLEA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=11792842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Firmicutes, Bacillus/Clostridium group; Clostridia, Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                      77 SDYHPSCKY-----TAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 LSLEVIĆCSTSG----EKNTINIPIEKSREEEKSKDEEEYIDKISSTIVNMSVDGSIKNM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPE0042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 IHVETLGCFSAGLPKTEANWVNVISD------LKKIEDLIQSMHIDATLYTE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein CPE0042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8XPC3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8XPC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 -----DSFVHIVDMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 21.9%;
                                                                                              Burr B.;
                                                                                                                                                       Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.7%; Score 89; DB 16; Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28; Mismatches
                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AD25C70C57665B3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                624 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 0.51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 AA.
                                                                                                                                                              core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50; Indels
                                                                                                                                                                             Tracheophyta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36; Caps
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Job time : 64.5 secs

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Q8W9S7
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Best Local S
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SEQUENCE 624 AA; 69815 MW; B52836B46EFAF782 CRC64;
                         2
                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                      Matches
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
NADH dehydrogenase subunit 2 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 ANNSLSSNGNVTESGCK-------BCEELEEKNIKEFLDSF---VHIVDMEI 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 LCNAQYADSKVESRSLVAKŚASIQTVVĆĖPYAGGVIELGVTDLVŠKDPGLIHRVKSLLLD 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 10.6%; Score 88.5; DB 10; Length 624; Local Similarity 24.0%; Pred. No. 2.9; hes 29; Conservative 23; Mismatches 44; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8W9S7
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21624446; PubMed-11752187;
Turmel M., Otis C., Lemieux C.;
Turmel Complete Mitochondrial DNA Sequence of Mesostigma viride
The Complete Mitochondrial DNA Sequence of Mesostigma viride
Identifies This Green Alga as the Earliest Green Plant Divergence and
Predicts a Highly Compact Mitochondrial Genome in the Ancestor of All
Green Plants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 APETIT--GNINDVACPGLGPNEIESELSPFLGCEQLERGSPNEISDGFEPNOPAEDPFV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 LIQSMHIDATLYTESDVHPSCKVTAMKCF-----LLELQVISLESGDASIHDTVENLIIL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesostigmatales; Mesostigmataceae; Mesostigma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Mesostigmatophyceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 N 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 N 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesostigma viride.
                                                                                                                                                                                                                                                                                                         STRAIN-NIES-296; Lemieux C.; Turmel M., Otis C., Lemieux C.; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF353999; AAL36732.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=41882;
                                                                                                                                                                                                                                                InterPro: IPR001750; Oxidored_gl.
pfam; pF00361; oxidored_gl; 1.
oxidoreductase; Mitochondrion.
SEQUENCE 497 AA; 55214 MW; 049
                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                        143 SIELOSECFELLAASRRNSEFSTEAGLKYFLLGAFSSGLFLFGSSFIYGFTGQTSLEELA 202
                                                                                                                                                                                                                                                                                                                                                                                                    1. Biol. Evol. 19:24-38(2002).
                             125 NGNVTESG 132
                                                            203 KA-----TES------LFALE------SVYNNESNGLIIGILFLSA 231
232 -GFLFKSG 238
                                                                                                                                                     10 SISIOCYLCLLL-----NSHFLTEAGIHVFILGCESAGLPKTEANWVNVISDLKKIEDLI 64
                                                                                           65 QSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSS 124
                                                                                                                                                                                  Match 10.5%; Score 87.5; DB 8; Length 497; Local Similarity 27.3%; Pred. No. 2.8; es 35; Conservative 22; Mismatches 34; Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                            0498D770D73DFA7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                497 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25; Gaps
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Search completed: February 20, 2003, 16:31:15

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Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 20000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                 A_Geneseq_101002:*

1: /SIDS2/gcgdata/ge
2: /SIDS2/gcgdata/ge
3: /SIDS2/gcgdata/ge
4: /SIDS2/gcgdata/ge
5: /SIDS2/gcgdata/ge
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8: /SIDS2/gcgdata/ge
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12: /SIDS2/gcgdata/g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            February 20, 2003, 16:27:07; search time 33 Seconds (without alignments) 654.139 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRISKPHLRSISIQCYLCLL.....NIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-855-313A-4
833
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/geneseqp_embl/AA1988_DAT:
/SIDS2/gcgdata/geneseq/geneseqp_embl/AA1988_DAT:
/SIDS2/gcgdata/geneseq/geneseqp_embl/AA1989_DAT:
/SIDS2/gcgdata/geneseq/geneseqp_embl/AA1990_DAT:
/SIDS2/gcgdata/geneseq/geneseqp_embl/AA1991_DAT:
/SIDS2/gcgdata/geneseq/geneseqp_embl/AA1992_DAT:
                                                                                                                                          /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

L 0 9 8 7 6 5 4 3 2 2 1	Result
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	Score
100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	% Query Match
162 162 162 162 162 162 162 162 162	Query Match Length DB
16 16 17 17 17 18 18 18 19	DB
AAR83438 AAR6927 AAW09098 AAW07255 AAR98527 AAW37369 AAW01658 AAW3878 AAW33878	SUMMARIES ID
Human interleukin- Human II-15 Homo Simian epithelium- Human epithelium-d Human interleukin- Wild-type interleu Human interleukin- Simian epithelium- Simian epithelium-	

	4 U	44	43	7 + 2	a. ←	A 4	40	٥	38	37	36	G.	34) (L	3 0	با ر با د	J (J () N) () (27) V) (Д) t	2 10	27	21	20	10	18	17	16	15	14	ا ا د	11 12
	581	581	581	180	185	100	7 C	000	30 J	805	805	805	805	805	805	800	805	0 0	000	000	0 0	0 0 0	0220	0 40	000	p (ر ا ا ا ا	000	0 0	ر د د د د د د د د د د د د د د د د د د د	000	200	200	۵ ا ا ا	D ()	833
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	21																																			
	AAY523(T C C MY TI	PURCHANA	PAMOOO	AAR833	AAY548	AAB663	AAB620	AAY523	CR/XWW	201007	77007	AMPOR	AAR927	AARGRS	AAW072	AAW091	AAR66c	AAR834	ABB08	AAU779	AAW37	AAU77	AAU77	AAO14	AAU11	ABB08	AAU77	ABB08	AAB50	AAB66	AAB62	AAE0	AAY52	AAY78	AAB18
macure simian epit	imian epithel	ithelium	imian mature epi	Human interleukin-	n Interleukin	u in	umdn ETF (hETF)	יי פלידר	uman epitholius	n interiorist	n epithel	thelium	TD .	Simian interleukin	imian epithel	n epithelium	an IL-15. Ce	n	interl	n 1L-15 doub	L interleuk	an LL-15 singl	n IL-15	n inter	1-1	r numa	wild-ty	n inter	TL-15	n interle	an cir (Turet TedXI	an epitheli	undn inte	o acid sequen	

ALIGNMENTS

AAR83438 RESULT 1

AAR83438 standard; Protein; 162 AA.

AAR83438;

Human interleukin-15 precursor. 02-FEB-1996 (first entry)

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WPI; 1995-373556/48.
N-PSDB; AAT00526.
                           Anderson DM, Eisenman JR,
                                           (IMMV ) IMMUNEX CORP.
                                                            06-APR-1994;
                                                                          06-APR-1994;
                                                                                         19-OCT-1995.
                                                                                                         W09527722-A.
                         Rauch C;
                                                                                                                                                     Homo sapiens.
                                                                                                                                Peptide
                                                                                                                                                           Interleukin-15; epithelium-derived T-cell factor; T lymphocyte
                                                          94WO-US03793.
                                                                        94WO-US03793
                                                                                                                              Location/Qualifiers 1..48
                                                                                                                    /label= leader
                         Fung V, Grabstein KH;
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22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A simian species of IL-15 (sIL-15) was purified and its AA companies and cDNA sequence analysed (see AAR83309, AAR83436). AAR83436, AAR05254, AAR05255). Both the simian and the human ORFs encode AAR05254, AAR05255). Both the simian and the human ORFs encode a precursor polypeptide (AAR83438). The precursor of polypeptides at 48-AA leader sequence and a sequence encoding mature simian or human IL-15 polypeptides. The active encoding mature simian or human IL-15 polypeptides are disclosed in AAR83309 & simian and human IL-15 polypeptides are disclosed in AAR83309 & simian and human IL-15, that hybridise to probes defined by IL-15, including human IL-15, that hybridise to probes defined by Conna was deposited with ATCC on Feb. 19 1993 under ATCC 69245. Conna was deposited with ATCC on Feb. 19 1993 under ATCC 69245. IL-15 polypeptide. It is a generic sequence which encompasses both IL-15 polypeptide. It is a generic sequence which encompasses both IL-15 polypeptide. It is a generic sequence which encompasses both IL-15 polypeptide. It is a generic sequence which encompasses both IL-15 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
AAR66927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                         H
Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated DNA encoding polypeptide with mammalian IL-15 activity - which stimulates proliferation and differentiation of T cells, used for treating carcinoma(s), melanomas, etc. and viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 24; Page 28-29; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR66927 standard; Protein; 162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                         04-SEP-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                         Interleukin-15; IL-15; hIL-15; T-cell growth factor;
                                                                                                                                                                                                                                                                                                                                                                         Human IL-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR66927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVOMFINTS 162
                                                                                                                                                                                                                                                                                                                          antitumor; virucide.
                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                            ZA9402636-A.
                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
            (IMMV ) IMMUNEX CORP.
                                              18-APR-1994;
                                                                                                           28-DEC-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRISKPHLRSISIOCYLCLLLNSHFLTEAGIHVFILGCTSAGLPKTEANWVNVISDLKKI 60
                                                                             18-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDLIQSMHIDATLYTESDVHPSCKYTANKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                94ZA-0002636
                                                94ZA-0002636.
                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                /note= "active human IL-15"
                                                                                                                                                                                                                              /label= Sig_peptide
                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                  Mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 833; DB 1
pred. No. 2e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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0; Gaps

0

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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ωy
                                                                                                                              QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New purified interleukin-15 - which induces T cell proliferation and differentiation, used for the treatment of tumours and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anderson DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A SIL-15 probe was prepared from isolated simian interleukin-15 cDNA and used to screen a cDNA library generated from the LMTLH cell, line derived from human bone marrow stromal cells. Clone cell, line derived from human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ84584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rauch C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 24; Page 28-29; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-082473/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141.hETF encoded human IL-15.
                                                                                                                                                                                                                                                                                                                  SETF; African green monkey; CV1/EBNA cell; T-cell; B-cell; Jymphocyte; proliferation; differentiation; gastrointestinal;
                                                                                                                                                                                                                                                                                                                                                             Simian epithelium derived T cell factor precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW09098 standard; Protein; 162 AA
                                                             22-FEB-1995;
08-MAR-1993;
22-APR-1994;
                                                                                                                                                                                                                                                                                                        HTV infection; human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                         11-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  AAW09098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 SLSSNGNVTESGCKECEELEEKNIKEFLOSEVHIVOMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 SLSSNGNVTESGCKECEELEEKNIKEFLOSFVHIVOMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 100.0%; Score 833; DB 1 Local Similarity 100.0%; Pred. No. 2e-85; hes 162; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                               Cercopithecus aethiops.
                                                                                                                                                                         US5574138-A
                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 EDLIQSMHIDATLYTESDVHPSCKYTAMKCFLLELQVISLESGDASIHDTYENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRISKPHLRSISTOCYLCLLLNSHFLTEAGTHVFILGCESAGLPKTEANWVNVISDLKKI 60
                                                                                                                    08-MAR-1993;
                                                                                                                                                12-NOV-1996
                                    (IMMV ) IMMUNEX CORP.
              Anderson DM,
Rauch C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eisenman JR, Fung V,
                Eisenman JR, Fung V, Grabstein KH;
                                                                   93US-0031399.
94US-0233606.
                                                                                                                       93US-0031399
                                                                                               95US-0393305
                                                                                                                                                                                                                  /label= leader
49..162
                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                       /label= mature_sETF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grabstein KH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW07255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
         (IMMV ) IMMUNEX CORP
                                      08-MAR-1993;
                                                                08-MAR-1993;
                                                                                             03-SEP-1996
                                                                                                                         US5552303-A.
                                                                                                                                                                      Protein
                                                                                                                                                                                                                                             Epithelium-derived T-cell factor; simian; human; culture; proliferation; epithelial cell; differentiation; T-lymphocyte; African green monkey; primer; PCR; polymerase chain reaction; amplification; probe.
                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                 Human epithelium-derived T cell factor.
                                                                                                                                                                                                                                                                                                                                               05-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       AAW07255;
                                                                                                                                                                                                                                                                                                                                                                                                       AAW07255 standard; Protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The simian ETF (epithelium derived T cell factor) was isolated from African green monkey CVI/EBNA cell conditioned medium. The N-terminal sequence of the purified sETF was determined and then PCR fragment was amplified from CVI/EBNA DNA and was used as a probe to sequence. Mature sETF induces proliferation and/or differentiation sequence. Mature seTF induces proliferation and/or differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 SLSSNGNVTESGCKECEELEEKNIKEELQSEVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 SLSSNGNVTESGCKECEELEEKNIKEFLOSFVHIVOMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  malignancy and for treating HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of precursor or mature T cells and is useful for promoting long-term in vitro culture of T-lymphocytes and T-cell lines. It is used for treating gastrointestinal diseases including peptic ulcer, colitis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 1; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New epithelium derived T cell factor - induces proliferation of T and B cells, stimulates destruction of tumour and virus-infected \bar{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 EDLIQSMHIDATLYTESDVHPSCKVTANKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cells and protects against toxicity, partic. for treating intestinal disease and \ensuremath{\mathrm{HIV}} infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 EDLIQSMHIDATLYTESDVHPSCKYTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-517923/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRISKPHLRSISIOCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRISKPHLRSISIGCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                    93US-0031399
                                                             93US-0031399
                                                                                                                                           /note= "mature protein"
                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                      /note= "signal peptide"
                                                                                                                                                                 .162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 833; DB 17; Length 162; 100.0%; Pred. No. 2e-85; tive 0; Mismatches 0; Indels 0
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(IMMV ) IMMUNEX CORP
                                    22-FEB-1995;
                                                                  21-FEB-1996;
                                                                                                29-AUG-1996.
                                                                                                                               W09626274-A1
                                                                                                                                                                           Misc-difference 156\, mpreferred site for amino acid substn."
                                                                                                                                                                                                                                                                                  allograft; T-cell growth factor.
                                                                                                                                                                                                          Misc-difference 56
                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                     Interleukin-15; antagonist; mutein; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                               17-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                     Human interleukin-15.
                                                                                                                                                                                                                                                                                                                                                                                                         AAR98527;
                                                                                                                                                                                                                                                                                                                                                                                                                          AAR98527 standard; Protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the amino acid sequence of a human epithelium-derived T-cell factor (ETF). The gene was obtained using a 1.37 kb fragment of the corresp. African green monkey gene (AAT42242) as a probe to screen a cell line is derived from RNA derived from the IMTLH cell line. This stromal cell culture with psyshes. From a pool of about 1000 cDNA kD which is expressed by epithelial cells and stimulates proliferation and/or differentiation of precursor and/or mature T cells. The protein is themselved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 SLSSNGNVTESGCKECEELEEKNIKEFLOSFVHIVOMFINTS 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is therefore useful for promoting long term in vivo culture of T-lymphocytes and T-cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 21; Column 23-24; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 EDLIQSMHIDATLYTESDVHPSCKVTANKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-lymphocytes and T-cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated simian and human epithelium-derived T-cell factors - which stimulate the proliferation and/or differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson D, Eisenman J, Fung V, Grabstein K, Rauch C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRISKPHLRSTSTOCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRISKPHLRSISIOCYLCLLLNSHELTEAGIHVEILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 100.0%; Score 833; DB 1 Local Similarity 100.0%; Pred. No. 2e-85; es 162; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 AA;
                             95US-0392317.
                                                              96WO-US02520.
                                                                                                                                           /note= "preferred site for amino acid substn."
                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB_17; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETF is a protein of 15-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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And Human interleukin-15 (II-15) (AAR98527) is a T-cell growth factor. With the control of the predict of the p
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     symptoms of graft-versus-host disease and for prolonging allo:graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antagonists of interleukin-15 - are used to treat patients having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT36635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 25; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW37369 standard; Protein; 162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wild-type interleukin-15 (IL-15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 SLSSNGNVTESGCKECEELEEKNIKEFLOSFVHIVOMFINIS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                   Interleukin-15; IL-15; mutant; human; treatment; autoimmune disease; psoriasis; multiple sclerosis; rheumatic arthritis; immune response;
                                                                                                                                                                                        /note=
Misc-difference 149
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                           type 1 diabetes; AIDS.
                     WO9741232-A1
                                                                                                                    Misc-difference 156
                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 EDLIQSWHIDATLYTESDVHPSCKVTANKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRISKPHLRSISTOCYLCLLLNSHFLTEAGTHVFILGCESAGLPKTEANWVNVISDLKKI 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                        /note= "The specifications claims a substitution of
                                                                                                                                                                                                                                                                          /note= "signal sequence"
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                 /note= "The specifications claims a substitution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 833; DB 1
100.0%; Pred. No. 2e-85;
                                                                                                                                                                                                                        "mature IL-15 polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pettit DK;
                                                                                                                                                 Gln at this position to Asp"
                                                                            Gln at this position to Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 17; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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                                                   RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for suppressing the immune response in a patient. It can be used for treating autoimmune diseases such as rheumatic arthritis, type I diabetes treating autoimmune diseases such as rheumatic arthritis, type I diabetes or a rheumatic disease selected from systemic lupus erythematosus (SLE), or a rheumatic disease selected from systemic lupus erythematosus (SLE), or a rheumatic disease selected from systemic lupus erythematosus (SLE), dermatomyositis, selectederma, mixed connective tissue disease, selectederma dermatomyositis, garactic syndrome and Behcet's disease, It can also be used to treat Hashimoto's thyroiditis, Grave's disease, it can also be used for reducing the variety of injury. The mutant II-15 can also be used for reducing the viability of a cell that expresses a IL-15 receptor. It can also be used to diagnose a disease treatable with an IL-15 antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the wild-type interleukin-15 (IL-15) polypeptide. This wild-type sequence can be mutated at codon positions 149 and 156 to create a mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutant interleukin 15 polypeptide(s) - used for treating auto-immune diseases e.g psoriasis, multiple sclerosis etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAT97227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cellular events that normally occurs when the wild-type IL-15 is used specifically binds to a cell surface receptor. The mutant IL-15 is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IL-15 polypeptide. The mutant polypeptide is at least 90% identical to the wild type IL-15 and is capable of inhibiting at least one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Pages 55-56; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-549734/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                       AAW01658 standard; Protein; 162 AA
                                                                        glucose-intolerance; dyslipidaemia; rhabdomycosarcoma;
                                                                                         IL-15; interleukin-15; T-cell growth factor; proliferation; stimulate; muscle growth; differentiation; hypertrophy; treat; atrophy; wasting; skeletal; cardiac; muscle; congestive heart failure; diabetes-associated; skeletal; cardiac; muscle; congestive heart failure; diabetes-associated;
                                                                                                                                                                                                                                                     AAW01658;
                                                                                                                                                                                                                                                                                                                                                                                     Human interleukin-15
                                                                                                                                                                                                                                                                                                                                                                                                                           121 SLSSNGNVTESGCKECEELEEKNIKEFLOSFVHIVOMFINTS 162
W09637223-A1.
                                                                                                                                                                                                              18-MAR-1997 (first entry)
                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 EDLIQSMHIDATLYTESDVHPSCKVTANKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRISKPHLRSISTOCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLFKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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100.0%; Pred. No. 2e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 18; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
 19-JUL-1995;
08-MAR-1993;
22-APR-1994;
                                               19-JUN-1995;
                                                                       05-MAY-1998
                                                                                             US5747024-A.
                                                                                                                   Homo sapiens
                                                                                                                                      cytokine; growth factor.
                                                                                                                                                                           Human interleukin-15
                                                                                                                                                                                                 13-JUL-1998 (first entry)
                                                                                                                                                                                                                                           AAW53878 standard; Protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for treating atrophy, or wasting, in particular, skeletal and cardiac muscle atrophy. The compsns. further comprises a steroid, growth hormone and insulin-like growth factor. Congestive heart failure, muscle wasting and diabetes associated glucose-intolerance or dyslipidaemia, rhabdomycosarcoma and muscular dystrophy can all be treated by such
                                                                                                                                                                                                                                                                                                  121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is human interleukin-15 (IL-15), a known T-cell growth factor that can support proliferation of an IL-2-dependent cell line, CTLL-2. Compsns. contg. IL-15 to stimulate muscle growth, differentiation or hyperrrophy are claimed. The stimulation of muscle growth is useful
                                                                                                                                                                                                                                                                                                                         121 SLSSNGNVTESGCKECEELEEKNIKEFLOSFVHIVOMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 12; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muscle trophic compsn. contg. interleukin 15 congestive heart failure, muscle wasting etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grabstein KH, Ouinn LS,
                                                                                                                                                                                                                                                                                                                                             61 EDLIQSMHIDATLYTESDVHPSCKVTANKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                   61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                         1 MRISKPHLRSISIOCYLCLLLNSHELTEAGIHVEILGCESAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                       1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCESAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCAL
                                                                                                                                        interleukin-15; IL-15; T cell; B cell; proliferation; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1997-020939/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT58404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 AA;
94US-0233606
                       95US-0504042
                                             9508-0504042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0535733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-US06423
                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 833; DB 1: 100.0%; Pred. No. 2e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contg. interleukin 15 - for treating, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Troutt AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 18; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                  В
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
04-OCT-1996;
                                                   13-JAN-1998,
                                                                                                US5707616-A.
                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                 Simian
                                                                                                                                                                                                                                                                                                                                       Epithelium derived T-cell factor; ETF; simian; gastrointestinal disease; B-cell stimulation; epithelium; villi; CD4+; CD8+; T-cell stimulation;
                                                                                                                                                                                                                                                                                                                                                                                                                          Simian epithelium derived T-cell factor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAY-1998 (first entry)
                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW39185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW39185 standard; Protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is human interleukin-15 (IL-15), which can be used in the vaccine of the invention. The vaccine composition comprises an immunogenic amount of a vaccine antiqen (Ag) and an immunogenicity augmenting amount of IL-15. The composition is useful for enhancing the immunogenicity of a vaccine. The cytokine IL-15 is a potent of these cells and augments T cell mediated immune responses. The vaccine composition can sufficiently elicit an immune responses without being deficient antiques. Some vaccines do not elicit a strong immune response deficient antiques. Some vaccines do not elicit a strong immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and cannot provide sufficient protection on further exposure to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Column 5-6; 5pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of Interleukin-15 - to enhance immunogenicity of a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 EDLIQSMHIDATLYTESDVHPSCKVTANKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV23554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grabstein KH, Widmer MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRISKPHLRSISIOCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDLIQSMHIDATLYTESDVHDSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1998-285678/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
96US-0726817.
                                                                                                                                           /label= ETF
                                                                                                                                                                                   /label= leader sequence
                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0393305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 833; DB 1 100.0%; Pred. No. 2e-85;

 Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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AAY03756
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-FEB-1995;
08-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 radiation therapy induced enteritis (gut toxicity), mucositis, peptic radiation therapy induced enteritis (gut toxicity), mucositis, peptic ulcer disease, gastroenteritis and colitis, villus atrophic disorders, malignancy and inflammatory bowel disease. ETF polypeptides may also be useful in the treatment of human immunodeficiency virus (HIV) and useful in the treatment of human immunodeficiency virus (HIV) and CD8+ HIV-associated disease due to their ability to stimulate CD4+ and CD8+ cells. Biologically active ETF may be used to treat a variety of other cells. Biologically active ETF may be used to treat a variety of other diseases or conditions where T-cell or B cell stimulation is desired.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treatment or prevention of gastrointestinal diseases - by administering epithelium-derived T-cell factor polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a full length simian epithelium-derived T-cell factor (ETF) which is used in a method for treating or preventing gastrointestinal disease. These polypeptides have particular application in the treatment of gastrointestinal disorders associated with disruption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Column 35-38; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAV02873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anderson DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rauch C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                  Simian epithelium-derived T-cell factor (ETF) precursor polypetide.
                                                                                                                                                                                                                                                                                                                                                                             AAY03756 standard; Protein; 162 AA
                                                                                                                                                                           Epithelium-derived T-cell factor; ETF; immunoassay; enteritis; ulcer; T cell proliferation; gastrointestinal disease; mucositis; colitis; gastroenteritis; villus atrophy; malignancy; inflammatory bowel disease; human immune deficiency virus; tumour; simian.
                                                                                                                                                                                                                                                                                                                                          AAY03756;
                                                                                                                                                                                                                                                                                                         10-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 SLSSNGNVTESGCKECEELEEKNIKEFLOSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                  04-OCT-1996;
                                                                     06-APR-1999
                                                                                                                                               Mammalia.
 22-FEB-1995;
                                                                                                          US5892001-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 EDLIOSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWUNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1998-100295/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eisenman JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0393305.
93US-0031399.
94US-0233606.
     95US-0393305
                                      96US-0725969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 833; DB 1: 100.0%; Pred. No. 2e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epithelium or villi such as chemotherapy- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fung V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grabstein KH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 19; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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PI XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cc diagnostic and therapeutic agents, e.g. when conjugated to toxins (or cc their precursors) or radionuclides. ETF induces proliferation and/or cc differentiation of T cells (or their precursors), e.g. for use in cc differentiation of T cells (or their precursors), e.g. for use in cc gastrointestinal disease (e.g. enteritis or mucositis induced by caption the trian disease (e.g. enteritis or mucositis induced by continues than disease (e.g. enteritis or mucositis induced by chemotherapy or radiation, peptide ulcer, gastroenteritis, colitis, cc villus atrophy, malignancy and inflammatory bowel disease, to treat cc villus atrophy, malignancy and inflammatory bowel disease, or cc human immune deficiency virus infection or associated disease, or cc proliferation, secretion of immunoglobulins or certain cytokines, proliferation, secretion of immunoglobulins or certain cytokines, proliferation, secretion of immunoglobulins or certain cytokines, cc increased anti-infectious disease immunity, induction of T-cell lytic captivity or increased destruction of tumour or virus-infected cells. The cc present sequence represents a simian ETF precursor polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
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                                                                                                                                                                    AC XXX DT XXX
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 162; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-1993;
22-APR-1994;
04-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a simian or human epithelium-derived T-cell factor (ETF) polypeptide antibodies are used, optionally when immobilized or labeled, to detec and quantify ETF in standard immunoassays. They may also be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibodies specific for epithelium-derived T-cell growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson DM, Eisenman JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated antibody that binds specifically to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Columns 35-36; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX29479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                     AAB18632;
                                                                                                                                                                                                                                                                                                                                                               AAB18632 standard; Protein; 162 AA
09-MAR-2000; 2000WO-US06067
                                                                                                                                                                      zalphal1 ligand; cytokine;
tumourigenesis; leukaemia;
                                                                                                                                                                                                                                Amino acid sequence of a human interleukin-4 helix A fragment
                                                                                                                                                                                                                                                                            22-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 SLSSNGNVTESGCKECEELEEKNIKEFLOSFVHIVQMFINTS 162
                                                                                   WO200053761-A2
                                                                                                                               Homo sapiens
                                           14-SEP-2000.
                                                                                                                                                                    tumourigenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRISKPHLRSISIOCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCESAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1999-253930/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0725969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-0031399.
94US-0233606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fung V, Grabstein KH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                             hematopoiesis; B cell tumour; interleukin-4
                                                                                                                                                                                               haematopoietic cell proliferation; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 833; DB 2
Pred. No. 2e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0

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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                       20-JAN-2000
                                                                                                  WO200002582-A2
                                                                                                                                          Homo sapiens.
                                                                                                                                                                 Interleukin-15; IL-15; antagonist; irritable bowel disease; IBD;
celiac disease; treatment; human.
                                                                                                                                                                                                                                     Human interleukin-15 (IL-15) protein sequence.
                                                                                                                                                                                                                                                                                                09-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                       AAY78595;
                                                                                                                                                                                                                                                                                                                                                                                   AAY78595 standard; Protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             toxin may be used for treating leukaemias and lymphomas. Antagonists against zalphall ligand are useful as research reagents for for inhibiting expansion, proliferation, activation and differentiation of cells involved in regulating hematopolesis. The zalphall ligand may virus, a parasite or a bacterium. The zalphall ligand may polymucleotides, antagonists, agonists and antibodies are also useful for the detection, diagnosis, prevention, and treatment of diseases for the detection, diagnosis, prevention, and treatment of diseases associated with a zalphall ligand genetic defect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents part of a human interleukin-4. It is used to produce fusion proteins with a human zalphall ligand. Zalphall ligand is a cytokine. The zalphall ligand is useful for stimulating the proliferation and development of haematopoletic cells in vitro and in vivo. Zalphall ligand polynucleotides can be used as primers or probes for cloning the zalphall ligand-saporin fusion useful for treating tumourigenesis. A zalphall ligand-saporin fusion to vivo many harman and lumphamae antergenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; Page 253-254; 256pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human cytokine, designated zalphall ligand, useful for stimulating the proliferation and/or development of haematopoietic cells in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and in vivo, and for treating tumourigenesis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-565600/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAR-1999;
11-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnston JV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRISKPHLRSISIOCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRISKPHLRSISIOCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 100.0%; Score 833; DB 2
Local Similarity 100.0%; Pred. No. 2e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDLIQSMHIDATLYTESDYHPSCKYTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Presnell SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nelson AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0142013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0264908.
99US-0265992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sprecher CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dillon SR, Hammond AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Holly RD, Gross JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                     AAY52308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                   Protein
                                                                                                                                                                                                                                                       ETF; epithelium-derived T-cell factor; T-cell; T-lymphocyte; proliferation; differentiation; growth factor; precursor; mature; CD8+; gastrointestinal; epithelium; cell culture; treatment; HIV;
                                                                                                                                                     Mammalia
                                                                                Peptide
                                                                                                                                                                                          inflammatory bowel disease; villus atrophic disorder; enteritis; chemotherapy; radiotherapy; gut toxicity; cancer; side effect;
                                                                                                                                                                                                                                                gastrointestinal disease; gastroenteritis; colitis;
                                                                                                                                                                                                                                                                                                                                                       Simian epithelium-derived T-cell factor (ETF) precursor protein
                                                                                                                                                                                                                                                                                                                                                                                                                    09-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY52308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY52308 standard; Protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antagonists. The antagonists are preferably muteins of IL-15, antibodies against II-15 or IL-15 molecules bound to chemical groups that interfere with the ability of IL-15 to effect a signal transduction through either the alpha or the gamma subunit of the IL-15 receptor complex. The IL-15 antagonists of the invention can be used to treat irritable bow disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the human interleukin 15 (IL-15) amino acid sequence. The IL-15 nucleotide sequence and the protein encoded by it can be used to determine and create antagonists of IL-15. An antagonist of IL-15 can be used for treating an inflammatory bowel disease (IBD). The invention relates to the treatment of cellam cdisease using IL-15 can be used for treating an inflammatory bowel disease (IBD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 69; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease, particularly celiac disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of antagonists of interleukin-15 for treating an inflammatory bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ90032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-171080/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 EDLIQSMHIDATLYTESDYHPSCKYTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Londei M, Quaratino S, Maiuri L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KENN-) KENNEDY INST RHEUMATOLOGY MATHILDA & TER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRISKPHLRSISIOCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 AA;
                                                                                             Location/Qualifiers
                                          /note= "Leader peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98GB-0014892
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                                .162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 833; DB 2
100.0%; Pred. No. 2e-85;
"Mature simian ETF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB_21; Length 162;
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0,

Indels

0;

mature; CD4+;

IJ

밁 Qγ ₽ Q В

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SOX
                                                                                                                                  RESULT 14
AAE08576
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                                                                                                                                                                                                                                                                                                                                          Вb
                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                       Db
                                                                                                                                                                                                     Дb
X E X B X A X
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and T-cell lines. EFF can be used for treating HV infection.
HIV-associated diseases, and other diseases or conditions where
HIV-associated diseases, and other diseases or conditions where
stimulation of T-cell proliferation would be desirable e.g., it
stimulation of T-cell proliferation would be desirable e.g., it
could be used to augment the destruction of tumour cells or
could be used to augment the destruction of tumour cells or
virally infected cells. EFF may also be used to treat or prevent
virally infected cells. EFF may also be used to treat or prevent
gastrointestinal disease, including chemotherapy and radiotherapy
associated enteritis, gastroenteritis, colitis, inflammatory bowel
associated enteritis (gut toxicity) results in bleeding and sepsis due
to gastrointestinal flora entering the blood, and thus can limit the
dosage of therapeutic agent administered to a cancer patient. EFF may
thosefore he mead to increase the tolerance and cancer patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5985262-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rauch C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth factor which stimulates precursor or mature CD4+ and CD8+ Tlymphocytes to proliferate and differentiate. It also promotes proliferation of the gastrointestinal epithelium. The protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents simian epithelium-derived T-cell factor (ETF) precursor protein. ETF (AAY52309) is a previously unidentified T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Columns 35-38; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stimulation of T-cells in human immunodeficiency virus infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAZ38244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therefore be used to increase the tolerated doses radiotherapy and
                Human interleukin 15 (IL-15) protein
                                                  15-NOV-2001 (first entry)
                                                                                   AAE08576;
                                                                                                                     AAE08576 standard; Protein; 162 AA
                                                                                                                                                                                                       121 SLSSNGNVTESGCKECEELEEKNIKEFLOSFVHIVOMFINTS 162
                                                                                                                                                                                                                                     121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                       61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                        1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWYNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be used to promote long-term in vitro culture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-022267/02.
                                                                                                                                                                                                                                                                                                        EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fung V, Eisenman JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0233606.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0031399
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                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 833;
100.0%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grabstein KH,
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       2e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anderson DM;
                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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We drug screening; anthropological lineage; peternity testing; HIV; kW drug screening; and screening; HIV; kW drug screening; Av 200158914-A2.

XX Da - FEB - 2001 2001W-0180455.

XX Da - FEB - 2001 2001W-0181055.

XX Amastasio AP, Chew A, Denton RR, Nandabalan K, Stephens JC; PR R - FSDB; ADJ14455.

XX Avel polynuclectides comprising one of 11, PSI - PSI1, single nucleotide PR Polynorphisms in human interleukin-15 gene and useful for treating Pr Polynorphisms in human interleukin-15 protein. IL-15 gene is 2010-522460/57.

XX WPI; 2001-522460/57.

XX WPI; 2001-5
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94
                                                                    В
                                                                                                  2
                                                                                                                                       Db
                                                                                                                                                                       Οy
                                                                                                                                                                                                         Matches 162; Conservative
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                              Sequence
121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHTVQMFINTS 162
                                  121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                      61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                         1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                     1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                    EDLIQSNHIDATLYTESDVHPSCKVTANKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                    162 AA;
                                                                                                                                                                                                                                100.0%; Score 833; DB 2
100.0%; Pred. No. 2e-85;
                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                       DB 22; Length 162;
                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                              0; Gaps
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                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                      therapy and chemotherapy agents which are limited by gastrointestinal toxicity; and for treating HIV and HIV-associated diseases. The antibodies are further used to treat a variety of other diseases or T-lymphocytes and Blymphocytes, or the secretion of immunoglobulin Blymphocytes, to augment anti-infectious disease immunity, to induce CTL, or cells infected with virus. The present sequence represents the
                                                                                                                     Sequence
                                                                                                                                                                                                                                                          The invention relates to simian and human epithelium-derived T-cell factor (ETF) polypeptides. Antibodies that specifically bind to the ETF polypeptides are used for treating or preventing gastrointestinal disease, such as chemotherapy and radiation therapy-induced enteritis and mucositis, peptic ulcer disease, villus atrophic diseases and inflammatory bowel disease; for increasing tolerated doses for radiation therapy human disease; for increasing tolerated doses for radiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-FEB-1995;
04-OCT-1996;
08-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                        New antibodies that specifically binds epithelium-derived T-cell factor polypeptide useful for e.g. treating or preventing gastrointestinal diseases, HIV and HIV-associated diseases, augmenting destruction of
                                                                                                                                                                                                                                                                                                                                                                   Example 1; Column 35-36; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAF57017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grabstein KH, Anderson DM, Eisenman JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Epithelium-derived T-cell factor; ETF; simian; human; enteritis; gastrointestinal disease; mucositis; peptic ulcer; cytostatic; villus atrophic disorder; inflammatory bowel disease; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simian ETF (SETF) polypeptide.
                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia.
               1 MRISKPHLRSISIOCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB62012 standard; Protein; 162 AA
2001-217801/22.
                                                                                                                  162 AA;
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiviral; T-lymphocyte stimulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-0393305.
96US-0725969.
93US-0031399.
94US-0233606.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "leader sequence" 49..162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                             100.0%; Score 833; DB 2
100.0%; Pred. No. 2e-85;
                                                     0;
                                               Mismatches
                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fung V, Rauch C;
                                               0;
                                          Indels 0; Gaps
                                                                         Length 162;
                                            0;
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Db 1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60

Qy 61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120

Db 61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120

Qy 121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHTVQMFINTS 162

Db 121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHTVQMFINTS 162

Search completed: February 20 202 122 125
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Search completed: February 20, 2003, 16:28:24 Job time: 34 secs

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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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2: pir2:*
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                  AII1174
T34325
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FUN26 protein - ye
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interleukin-15 - m
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RESULT 2 Interleukin-15 - mouse C:Species: Mus musculus (house mouse) C:Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change C:Accession: I49124 R:Andderson, D.M.; Johnson, L.; Glaccum, M.B.; Copeland, N.G.; G Genomics 25, 701-706, 1995 A:Title: Chromosomal assignment and genomic structure of Il15. A:Reference number: A56005; MUID:95278940; pMID:7759105 A:Accession: I49124 A:Status: preliminary A:Molecule type. MUND:	RESULT 1 A53484 Interleukin-15 precursor - green monkey C:Species: Cercopithecus aethiops (green monkey, grivet) C:Date: 10.Sep-1999 #sequence_revision 10-Sep-1999 #text_change C:Accession: A53484 R:Grabstein, K.H.; Elsenman, J.; Shanebeck, K.; Rauch, C.; Srin Science 264, 95-968, 1994 A:Title: Cloning of a T cell growth factor that interacts with 1 A:Reference number: A53484 MOID:94233380; PMID:8178155 A:Accession: A53484 A:Residues: n-162 <gra> A:Status: nucleic acid sequence not shown A:Residues: 1-162 <gra> A:Residues: 1-162 <grap #status="" <mat="" a:cross-references:="" a:note:="" c:reywords:="" c:superfamily:="" complete="" f:49-162="" factor="" gb:u03099;="" growth="" interleukin-15="" is="" nid:9493521;="" not="" pidn:aaa18416.1;="" pii="" predicted="" product:="" shown="" the="" translation=""> F:83-133,90-136/Disulfide bonds: #status predicted <mat> F:83-133,90-136/Disulfide bonds: #status predicted Ouery Match Best Local Similarity 96.3%; pred. No. 5.9e-67; Matches 156; Conservative 1; Mismatches 5; Indels Ouery Match I </mat></grap></gra></gra>	ALIGNMENTS	30 76 9.1 938 2 T41932 31 75.5 9.1 670 2 E86164 32 75.5 9.1 1729 2 A49120 33 75.5 9.1 1313 2 T26954 34 75.5 9.1 1336 2 C86820 35 75 9.0 130 2 C86820 36 75 9.0 468 2 152418 37 75 9.0 468 2 152418 38 75 9.0 820 2 T05602 39 75 9.0 849 2 C97303 40 75 9.0 1021 2 C97303 40 75 9.0 1021 2 E84688 41 74.5 8.9 387 2 E84688 42 74.5 8.9 598 2 F75212 43 74.5 8.9 617 2 D96978 44 74.5 8.9 617 2 S64403
nge 16-Jul-1999 ; Gilbert, D.J.; Jenkins,	t) C.; Srinivasan, S.; Fung, V.; C.; Srinivasan, S.; Fung, V.; Els with the beta chain of the plant of the pl		hypothetical prote F15K9.10 protein - fibroblast growth hypothetical prote SEC3 protein - yea hypothetical prote acyltransferase (E cytochrome P450 - hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote glutamine fructose hypothetical prote glutamine fructose hypothetical prote glutamine fructose hypothetical prote glutamine fructose hypothetical prote glutamine fructose hypothetical prote

A; Molecule type: mRNA

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A;Cross=references: EMBL:U14332; NID:g984941; PIDN:AAA75377.1; PID:g984942
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A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: H97846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein RC1176 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
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A; Residues: 1-433 < KUR>
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                                                                                                                                             C:Species: Saccharomyces cerevisiae
C:Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 29-Oct-1999
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 29-Oct-1999
                                                                                                                                                                                              FUN26 protein - yeast (Saccharomyces cerevisiae) N;Alternate names: protein YAL022c
A; Description: Sequencing of Chromosome I from Saccharomyces cerevisiae: analysis of a A; Reference number: 836711
                                                       R;Ouellette, F.; Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, B.; Fortin, N.; submitted to the EMBL Data Library, January 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TLSSNKNVAESGCKECEELEEKTFTEFLQSFIRIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ESLIQSIHIDTTLYTDSDFHPSCKYTAMNCFLLELQVILHEYSNMTLNETVRNVLYLANS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 GDASIHDTVENLIILANNSLSSNGNVTES-----GCKECEELEEKNIKEFLQSFVHIV- 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKILKPYMRNTSISCYLCFLLNSHFLTEAGIHVFILGCVSVGLPKTEANWIDVRYDLEKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 GTASI---LSQLYKVMNDYIFSQGNITETSGADFLGLNECTKEEAMSALQNYNAYTETLI 174
                                                                                                                                                                                                                                                                                                                                                                          175 PRESFINT 182
                                                                                                                                                                                                                                                                                                                                                                                                                              156 -- QMFINT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 SISIQCYLCLLLN------SHFLTEAGIHVF-----ILGCFSAG--LPKTEANWV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 NIEQSFNESPNDFSILHQECNNGLNIPINNIFIDAENNPH------ILLQQTVTPHQN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 NVISDLKKIEDLIQSMHIDA-----TLYTESDVHPSCKVTAMKCFLLELQVISLES 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 11.6%; Score 96.5; DB 2; Length 433; Local Similarity 19.7%; Pred. No. 0.37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 NINFKCVMPIFSNEIVSRLSGNVSHIIHKLSSTIFSSVYSTVEGAFKKGYIVDNTQCNWK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.2%; Score 626; DB 2; Length 162; 72.8%; Pred. No. 1.8e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66; Indels 47;
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A; Molecule type: DNA
A; Residues: 1-517 < OUE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F:412-428/Domain: transmembrane *status predicted <TM7> F:445-461/Domain: transmembrane *status predicted <TM8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;344-360/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;218-234/Domain: transmembrane *status predicted <TM4> F;245-261/Domain: transmembrane *status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;155-171/Domain: transmembrane #status predicted <TM3>
F;177-193/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Keywords: transmembrane protein
F:79-95/Domain: transmembrane #status predicted <TM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: SGD:S0000020; MIPS:YAL022c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: SGD: FUN26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:L05146; NID:g171851; PIDN:AAC04935.1; PID:g171853; MIPS:YAL0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S36712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 1L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein ORF8 - Melanoplus sanguinipes entomopoxvirus (isolate Tsucon) C:Species: Melanoplus sanguinipes entomopoxvirus A:Variety: isolate Tuscon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 C;Accession: T28188 R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L. J. Virol. 73, 533-552, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: isolate Tuscon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AF063866; NID:g4049647; PIDN:AAC97859.1; PID:g4049899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-500 <AFO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: T28168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: The genome of Melanoplus sanguinipes entomopoxvirus A; Reference number: Z20484; MUID:99102612; PMID:9847359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 YLVLSIFTTFVVTLVFPVFASATYVTGLPLSNAQYIPLIFTLWNLGDLYGRVTADWPMFR 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     461 TNGHVISMSFMKVPEQLDNDDEKEAAGGFTNI---FVST 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 SNGNV-TESGCKECEELEEKNIKEFLQSFVHIVQMFINT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403 DQKETERKTEIYSLLRVAAIPLELMETAITSSSSGDEEHNGSV--IVDLCYMLLQELEGV 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 YLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKIEDLIQSMHIDATLYT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 ESDVHPS-----CKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS----- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                   149 NECKII-DFKFLESLINLEILDVSYNKNSNIYECTLPISLIELKCISCKIIDFKFLESLI 207
                                             208 NLEILDVSSNEYSNISDCKLPVSLIKLNCEFCYIYDFKFLETLNNIKIL NISYNKNSNI 266
129 TESGCKECEELEEKNIK------EFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                      49 NWVNVISDLKKIEDLIQSMHIDATLYTESDVHP-----SCKVTAMKCF--LL 93
                                                                                                                                                                                                                                                         90 TYKCKLSSLLKNINCNECKTIDEKEL-ESLINLEILDISYNKNSNIYKCKLSSLLKNINC 148
                                                                                                      94 ELQVISLESGDAS-----
                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                            3 ISKPHLRSI--SIQCYLCLLLNSHFLTEAGIHVFILG-----C-FSAGLPKTEA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40;
                                                                                                                                                                                                                                                                                                                                                                     49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Conservative 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.4%;
25.2%;
                                                                                                                                                                                                                                                                                                                                                                                            10.6%; Score 88.5; DE 21.8%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 95; DB 2
Pred. No. 0.63;
                                                                                                              -IHD-----TVENLIILANNSLSSNGNV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 500;
                                                                                                                                                                                                                                                                                                                                                                              60; Indels 73; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71; Indels
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C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C:Accession: AD1895
R:Kaneko, T.: Nakamura, Y.: Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-1799 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB72667.1; PID:g17130055; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: alr0710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Wolff, G.; Plante, T.; Lang, B.F.; Kueck, U.; Burger, G.
J. Mol. Biol. 237, 75-86, 1994
A;Title: Complete sequence of the mitochondrial DNA of the chlorophyte alga Prototheca A;Reference number: Z17373; MUID:94180393; PMID:8133522
A;Accession: T11943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Prototheca wickerhamii mitochond C:Species: mitochondrion Prototheca wickerhamii 2 - Prototheca wickerhamii mitochond C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: nad2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U02970; NID:g467843; PID:g467875; PIDN:AAD12662.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                            1669 NYGDLPLVNCFPGQLNQVFMNTLANATDALEEANIGKSFAEITAHPNRITITTS 1722
                                                                                                                                                                                                      1609 AMIMACNRLENISTSLRTFSRADKDYKVKFNLHEGIDSTILILKHRLKANQQHPAIEVIT 1668
                                                                                                                                                                                                                                                                                                                     1552 LGFISATLQQTKPNFADITEHLKLYQENLENPNREIQDHAKEMDLDFLL---EDLPKTID 1608
                                                                                                                                                    126 -- GNVTESGC-------KECEELEEKNI-KEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                              85 VTAMKCFLLE-----LQVISLESGD----ASIHDTVENLIILANNSLSSN------- 125
                                                                                                                                                                                                                                                                                                                                                                             36 LGCFSAGLPKTEANWVNVISDLK------KIEDLIQSMHIDATLYTESDVHPSCK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 LQSLSFYVLAALKRNSEFATEAGLKYFLLGAFSSGL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 10.2%; Score 85; Local Similarity 22.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 S-----DCKKLPVSLIKLNCGYCYTYDFKFLEPLINLQKLNISSN 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 LRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGL 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     28; Mismatches 57; Indels 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 1799;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
N\text{-ethylammeline chlorohydrolase [validated] - Rhodococcus corallinus}
                                                                                                                                                                             D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Cross-references: GB:L03789; NID:g173313; PIDN:AAA61343.1; PID:g173314 A:Note: sequence extracted from NCBI backbone (NCBIN:123574, NCBIP:123576) C:Superfamily: myb-related protein REB1; myb DNA-binding repeat homology C:Keywords: DNA binding; nucleus; transcription regulation F:333-382/Domain: myb DNA-binding repeat homology <NYB>
                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-595 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R:Morrow, B.E.; Ju, Q.; Warner, J.R.
Mol. Cell. Biol. 13, 1173-1182, 1993
A:Tille: A bipartite DNA-binding domain in yeast Reblp.
A:Reference number: A48077; MUID:93140755; PMID:8423784
A:Accession: A48077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C;Accession: A48077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myb-related protein REB1 - yeast (Kluyveromyces marxianus var. lactis)
C:Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Morrow, B.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Introns: 51/2; 122/2: 161/3; 181/3; 214/3; 328/1; 401/3; 458/3; 544/3; 596/2; 774/2
A:Note: T4F9.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein 74F9.30 - Arabidopsis thaliana %;Alternate names: protein 74F9.30 C:Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: cultivar Columbia; BAC clone T4F9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: AL049523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-928 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: T04192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the Protein Sequence Database, March 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Keference number: Z15260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                           235 NDDQQDDVSNLIQEAAAKASHIINPATQSNGKSFDESEEEALEQFIKEYQKI 286
                                                                                                                                                                                                104 DASIHDTVENLIILANNSLSSNGN-VTESGCKECEELEEKNIKEFLQSFVHI 154
                                                                                                                                                                                                                                                       183 PKKEKSEERSYGDLSNIDDHVDDVSVSGS1PSQVRLKKTAEVLP------KVLSSESH 234
                                                                                                                                                                                                                                                                                                               44 PKTEANWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 NLIILANNSLSSNGNVTES 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 SIVTIAGGPTLSNGHSTTS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 DPLSYKSLEE--SSLHMDQDTLVEVDGLSSSSQSAMSSTGNELALVPLEPS-----R 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 YTRSYSVEVYPLCLMLTDGRDESRTASIRELYEKVCAMTGVPQEKAHIWDYFDKRKNGLL 196
                                                                                                                                                                                                                                                                                                                                                                                                         Match 10.0%; Score 83.5; Di Local Similarity 25.0%; Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 D----LKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 HLRSISIOCY-LCLLL---NSHFLTEAGIHVFILGCFSAGLPKTEAN-W-----VNVIS 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 10.1%; Score 84; DB 2; Length 928; Local Similarity 25.9%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-Apr-1
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                                                                                                                                                                                                                                                                                                                                                                                Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 595;
                                                                                                                                                                                                                                                                                                                                                                    51; Indels
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Ъ QΥ В Qγ

Gaps

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N:Alternate names: s-triazine hydrolase
C:Species: Rhodococcus corallinus
C:Date: 18 Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-Jul-2000
C:Accession: T46666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: Z23125; MUID:96011356; PMID:7592318
A;Accession: T46666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erbicide atrazine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: involved in atrazine degradation [validated, MUID:96011356] C;Superfamily: Aquifex aeolicus N-ethylammeline chlorohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: tissue lib NRRL 15444B C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:L16534; NID:g294669; PIDN:AAA90931.1; PID:g294671
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A; Residues: 1-477 <SHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein C0760c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: Z18935
A; Accession: T18501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: T18501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: C0760c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL; 298551; NID:e1331903; PID:e1331922; PIDN:CAB11140.1
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                                                                                                                                                                                                                                                                                    Qy
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hypothetical protein RO3H4.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
                                                                                                                                                                                      Qy
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Bacteriol. 177, 5748-5755, 1995
Title: Cloning and expression of the s-triazine hydrolase gene (trzA) from Rhodococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 TYGIGTDDANCNDSVNLISDMKVLALIHRAAHRDASIITPEKIIEMATIDGARCIGMADQ
                                                                                                                                                                                                                                                                                                                                         2344 NNVNNINNVKNIVDINNYLVNNLQLNKDNDNIIIIKENILKLEKLGSCYLYIINRNLKEI 2403
                                                                                                                                                                                                                                           2404 QMLKNQILSLEESIKSLNEFINNLKNENEKNELIKINNFEEILKLKNNLQDNESCIQNLN 2463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381 IGSLEAGKRADIITLDLRHAQTTPAHDLAATIVFQAYGNEVNDVLVNGSV 430
                                                                                                                                             2464 NYLKKNEELNKINVKNIFKYKGYIIHLIQ 2492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 VISLESGDAS------IHDTVENLIILAN----NSLSSNGNV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 SAGLPKTEANW----VNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQ 96
                                                                                                                                                                                            131 SGCKECEELEE---KNIKEFLQSFVHIVQ 156
                                                                                                                                                                                                                                                                                                                                                                                     49 NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCF-------91
                                                                                                                                                                                                                                                                                       92 -LLELQVISLESGDASIHDTVENL-------IILANNSLSSNGNVTE--- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 22.19 les 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Conservative 22; Mismatches 41; Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 9.9%;
Similarity 23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-3394 <LAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.8%; Score 81.5; DB 2; Length 3394; 22.1%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                              29; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 82.5; DB 2; Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Gaps
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A

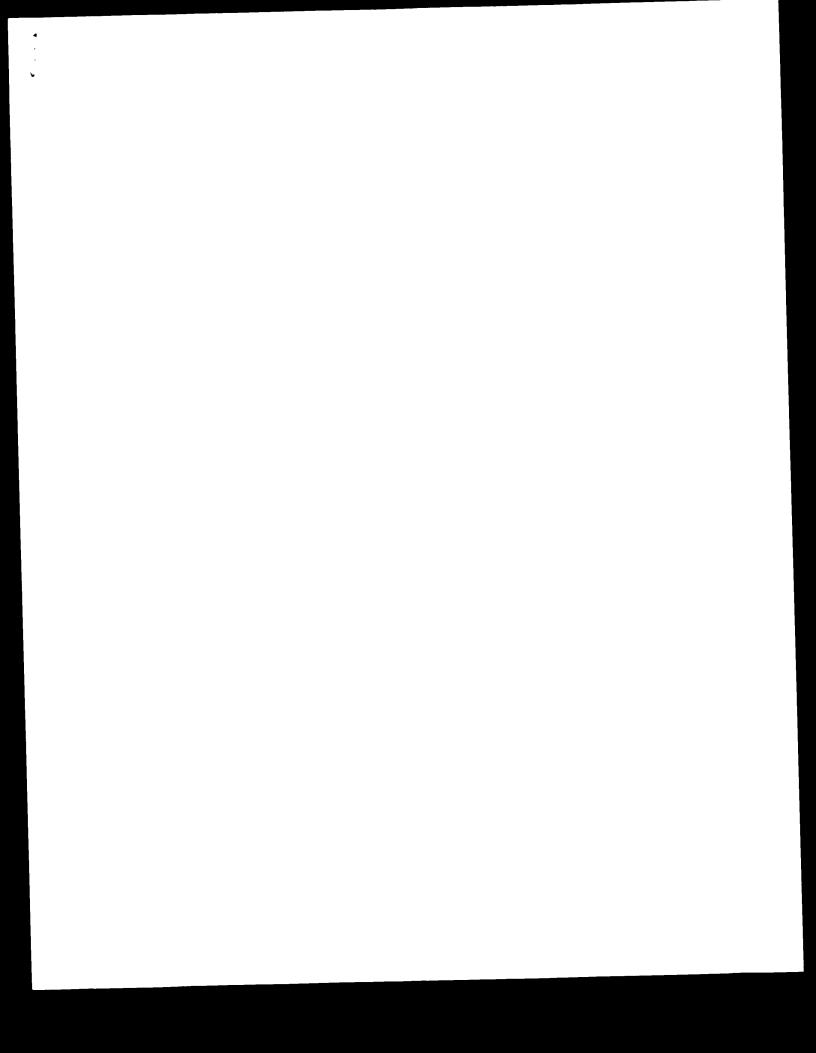
RESULT 14

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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 17-Nov-2000 C;Accession: T28886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain Bristol N2; clone R03H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U50300; PIDN:AAC48109.1; GSPDB:GN00023; CESP:R03H4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Accession: T28866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid R03H4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Bradshaw, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: CESP: R03H4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Geisel, C.; Kramer, J.; Smith, A.; Elliott, G.; O'Brien, D. submitted to the EMBL Data Library, July 1997 A;Description: The sequence of C. elegans cosmid C02A12. A;Reference number: Z16087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein CO2A12.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dр
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                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: V
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AF016415; NID:g2291123; PIDN:AAB65265.1; PID:g2291126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: T03854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                                                                                  Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics
B
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                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            570 MRCVKKREEKVKCKKCQFFDLSHVFVE-GDKYLTFDRDSLISYVDNTI----HLTSAGLK 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       625 LCQPVFENLAKEIMNN 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 9.7%; Score 80.5; DB 2; Length 642; Local Similarity 24.3%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 ECEELEEKNIKEFLQS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 NSHELTEAGIHVEILGCESAGLPKTEANWVNV-ISDLKKIEDLIQSMHIDATLYTESDVH 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 PSC-----KVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCK 134
                                                                                                                                                                                  543 VETLG----ALPTYPVNFLNAFLQNVMKSQEDMEKLHLNQKT-ADEDVKNEVKRFELAEK 597
                                                                                       598 RCK----KCQFIDLNPAFLEKGKYLTFD--RNSLL---SYLDNSGHLMPAAVKLCEPILE 648
649 KTI 651
                                             142 KNI 144
                                                                                                                                  82 SCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEE 141
                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translated from GB/EMBL/DDBJ
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ω
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                                                                                                                                                                                                                                                                                 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-922 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -642 <BRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                     9.7%;
25.2%;
                                                                                                                                                                                                                                                                                 24; Mismatches 43; Indels 25; Gaps
                                                                                                                                                                                                                                                                                                     Score 80.5; DB 2; Length 922; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57; Indels 19;
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                                                                                                                                                                                                                                                                                A:Gene: pep0
C:Superfamily: X-Pro aminopeptidase
                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB06898.1; GSPDB:GN0q
A:Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-364 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
C84047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Molecule type: DNA
A:Residues: 1-1070 <STO>
A:Cross-references: GB:AP000398; GSPDB:GN00144
                                                                                                                                                                                                                  Ouery Match 9.5%; Score 79.5; DB 2; Length 364; Best Local Similarity 22.4%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A;Reference number: A84930; MUID:20445173; PMID:10993077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exodeoxyribonuclease V (EC 3.1.11.5) 125 kD polypeptide [imported] - Buchnera sp. (straic: Species: Buchnera sp. (straic: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A: Experimental source: strain APS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
113 NLIILANNSLSSNGNVTESGCKECE-----ELEEKNIKE 146
                               92 KRNAVLTSCIVEAPRLTYARVQALQDAFPAIKLIDGEPFLMELR----K©KSAKELTTLK 147
                                                                      59 KIEDLIQSMHIDATLYTES-----DVHPSCKVTAMKCFLLELQVISLESGDASIHDTVE 112
                                                                                                              37 PHERLVSLLLEPEAEPCLICENMETSLVKEAGWTGETL-----GYSDIEDPWLLVRQAVE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        739 KKQFFYETKNIESFIQ 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 EE---LEEKNIKEFLO 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    697 HPSILVDQL-----LNYITL-----NFCFIGDQNLSYKENSKKITKYLCKKH 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  639 IPKT--NYLDNFNLLKKYPLIGDINLYQKYSYLFVQSLSCAEKYFYISYIGYSVKDESKV 696
                                                                                                                                                    6 PHLRSISI-----OCYLCLLLNSHFLTEAGIHVFILGCESAGLPKTEANWVNVISDLK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    579 LSSNYLKKISINILKKIFEYKYYDNNHEIFLDGVVNFCYPDSVCYIPFKVICMIGTDHTS 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 HPSCKVTAMKCFLLELOVISLESGDASIHDTVENLIILANNSLSSNGN---VTESGCKEC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 LPKTEANWVNVISDLKK---IEDL-----IQSM-----HIDATLYTESDV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 ISKPHLRSISIQCYLCLLL-----NSHFLTEAGIHVF------ILGCFSAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recC; BU453
                                                                                                                                                                                            36; Conservative 29; Mismatches 67; Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 9.7%; Score 80.5; DB 2; Length 1070; 1 Similarity 23.0%; Pred. No. 33; 45; Conservative 32; Mismatches 50; Indels 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50; Indels 69; Gaps
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Db 148 EAAALADYGVEVGVQAIQEGRSEIEILALIEYELKRKGVRD 188
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Search completed: February 20, 2003, 16:32:11 Job time: 26.5 secs



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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
             No.
                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
           833
8810
6620
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         Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 February 20, 2003, 16:27:07; Search time 16.5 Seconds (without alignments) 407.222 Million ceil updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRISKPHLRSISIQCYLCLL.....NIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-855-313A-4
833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd
                               VUZM_ACACA
YUZM_ACACA
YUZM_ACACA
YUZMACA
HSF1_CHLCK
CC10_SCHPO
V120_HSV7J
FGR1_DROME
SEC3_YEAST
LXD2_PHOLU
CPCJ_HUMA
ADMS_PYRAB
               CDAA_HUMAN
NU2M_CHOCR
                                                                                                                                                   REB1_KLULA
TRZA_RHOCO
TRPA_BUCSC
EX5C_BUCAI
RINI_RAT
HCYG_SEPOF
RPB1_DICDI
       PGBM_HUMAN
                                                                                                                                                                                                                                             IL15_PIG
IL15_BOVIN
IL15_SHEEP
                                                                                                                                                                                                                                                                                           IL15_HUMAN
IL15_MACMU
                                                                                                                                                                                                                                                                                                                      IJ
                                                                                                                                                                                                                 FU26_YEAST
                                                                                                                                                                                                                           IL15_MOUSE
IL15_RAT
                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                            P33261 homo sapien
Q9v249 p glucosami
P46682 saccharomyc
Q03018 saccharomyc
Q9zhe4 buchnera ap
 P98160
                                                                         Q07407
P333332
P23148
                                                                                                                              P29315
P56826
P35084
Q37376
P47166
                                                                                                                                                                           P31381
Q05950
Q052725
Q44604
P57528
                                                                                                                                                                                                                        Q95253 sus scrofa
Q28028 bos taurus
Q9xsj6 ovis aries
P48346 mus musculu
P97604 rattus norv
                                                                                                            P38529 gallus gall
P01129 schizosacch
                                                                                                                                                                                                                                                                  P48092 macaca mula
P40221 cercopithec
097687 felis silve
                                                                                                                                                                                                                                                                                             P40933 homo sapien
                                                                                                                                                                                                                                                                                                                 Description
                         3 saccharomyc
4 buchnera ap
                                                                      saccharomyc
photorhabdu
        homo sapien
chondrus cr
                                                                                                schizosacch
human herpe
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4 rattus norv
homo sapien
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dictyosteli
                                                                                          drosophila
                                                                                                                             saccharomyc
                                                                                                                                      acanthamoeb
                                                                                                                                                                         buchnera ap
                                                                                                                                                                                                   saccharomyc
kluyveromyc
                                                                                                                                                                  rattus norv
                                                                                                                                                                                          rhodococcus
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RESULT IL15_HU ID IL16_HU ID IL16 AC PAI AC	
SULT 1 ILIS_HUM. ILIS_HUM. ILIS_HUM. ILIS_HUM. ILIS_HUM. ILIS_HUM. ILIS_HUM. ILIS_HUM. ILIS_HUM. ILIS_HOME INCOME. ILIS_HOME. ILIS_HOM	34 35 37 39 41 42 43
5_HUMAN STANU PA0933; Q93058; C0438 O1-FEB-1995 (Rel. 3) O1-FEB-1996 (Rel. 3) O1-FEB-1997 (Rel. 3) O1-FET-1997 (Rel. 4) O1-FET-1996 (Rel. 4) O1-FET-1997 (Re	72.5 72.5 72.7 71.5 71.5 71.5 71.5 71.5 71.5 71.5
yan STAN Q93058; C43 3 1995 (Rel. 4) kin-15 precipiens (Human at Metazoa; Eutheria; Eutheria; Eutheria; Eutheria; Eutheria; Eutheria; Eutheria; ID=9606; FROM N.A. (9423380; pun K.K., Eises an S., Fung cancerieukin-2264:965-968 (FROM N.A. (7 Jandrig B 1960 N.A. (7 Jandrig B 1960 N.A. (7 FROM	888888888888 5555555555555555555555555
JARD; Creckles Created and Prima Pri	384 499 1265 456 456 521 807 1147 1733 248 248 1447 2832 552
. market of the end of	1
PRT; 11 2; 000440; 09UBA3 Created) Last Sequence up Last sequence Sor (IL-15). Last sequence Last	GRPR_HUM GSHR_PILA RPOD_CYA RPOD_CYA RINI_PIG RINI_PIG ROM_HUM PYMM_HUM NRDC_HUM NRDC_HUM NRDC_HUM NRDC_HUM NRDC_HUM NRDC_HUM NRDC_HUM NRDC_HUM NDVB_RHII THSB_SUL' ALIGN
16 IBA3; e upd on u ata; rhin orm) ORM) ORM) Bulf beck ichau ichau ichau ifin-li humm BB./ iin-li humm i J.M retab	GRPR_HUMAN GSHR_PLAFK RPOD_CYAPA RINI_PIG RINM_HUMAN PTMM_HUMAN NRDC_HUMAN NRDC_HUMAN NRDC_HUMAN NRDC_HUMAN NRDC_HUMAN NRDL_HUMAN NRDL_HUMAN NRDL_HUMAN NRDL_HUMAN NRDL_HUMAN NRDL_RHIME THSB_SULTO
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mo. Crisor Csor Csor Csor Csor Csor Csor Csor C	P30550 Q94655 P18120 P10679 Q00629 Q9212 Q13847 P043847 P20471 Q24735
aton A. A Process of A. A Proc	50 hc 55 pl 720 cy 75 su 75 ho 71 ho 50 sa 50 sa 71 rh
chain chain rms	homo sap plasmodi cyanopho sus scro homo sap homo sap homo sap charo drosophi homo sap saccharo gracharo gracha
	0 homo sapien 5 plasmodium 6 cyanophora 5 sus scrofa 5 sus scrofa 6 homo sapien 7 homo sapien 8 accharomyc 6 drosophila 1 homo sapien 8 sulfolobus

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Вþ
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                                                                                                                         Вþ
                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                       Matches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF TL-15-LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-18, INCLUDING IL-2R BETA AND PROBABLY IL-2R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "IL15 expression in human keratinocytes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sorel M.A., Jacques Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Epidermıs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U14407; AAA21551.1; EMBL; X91233; CAA62616.1; EMBL; X94223; CAA63914.1; EMBL; X94222; CAA63913.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytokine; Glycoprotein; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew;
                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003443; Interleukin_15.
Pfam; PF02372; IL15; 1.
                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                               VARSPLIC
                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                            PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                    CONFLICT
 121
                             121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: SECRETED (IL15-S48AA). IL15-S21AA IS NOT SECRETED, BUT RATHER IS STORED INTRACELLULARLY, APPEARING IN THE NUCLEUS AND CYTOPLASMIC COMPONENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE PRODUCTS: 3 ISOFORMS; IL15-S48AA (SHOWN HERE), IL15-S21AA AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: MOST ABUNDANT IN PLACENTA AND SKELETAL MUSCLE. IT IS ALSO DETECTED IN THE HEART, LUNG, LIVER AND KIDNEY. IL15-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAMMA BUT NOT IL-2R ALPHA
                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DATABASE: NAME=R&D Systems' cytokine source book: IL15;
WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=209"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE IL-15 FAMILY. DATABASE: NAME=R&D Systems' cytokine sou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S21AA IS PREFERENTIALLY EXPRESSED IN TISSUES SUCH AS TESTIS AND
                                                                                                                                                                                                        Local
                                                                                                                                                      1 MRISKPHLRSISTOCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                         1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSÄGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        600554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y09908; CAA71044.1; -. Z38000; CAA86100.1; -.
SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                             EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                          EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF031167; AAB97518.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGNC:5977; IL15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                        162 AA;
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                               30
49
83
90
127
                                                                                                                                                                                                                                                                      141
                                                                                                                                                                                                                                                        18086 MW;
                                                                                                                                                                                                        100.0%; Score 833; DB 1; 100.0%; Pred. No. 2.2e-69;

 Mismatches

                                                                                                                                                                                                                                                          E -> K (IN REF. 4).
; OCE0520C1D8379E2 CRC64;
                                                                                                                                                                                                                                                                                                                                 MRISKPHLRSISIQCYLCLLINSHFLTEAGIHVFILG -> MYLGTIDLCS (IN ISOFORM IL15-S21AA).
                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                     MRISKPHLRSISIOCYLCLLLNSHFLTEAGIHVFILGCFSA
                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                  INTERLEUKIN-15.
                                                                                                                                                                                                                                                                                                        GLPKTE
                                                                                                                                                                                                                                                                                       ISOFORM 3
                                                                                                                                                                                                                                                                                                      -> MDFQVQIFSFLLISASVIMSR (IN
                                                                                                                                                                                                                              Length 162;
                                                                                                                                                                                                                                                                                                                                                                     .) (POTENTIAL)
                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                    0;
                                                                                                                                                                                                    Gaps
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RESULT 2

RESULT 3

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IL15_MACMU
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                                                                                                                   рь
                                                                                                                                             QΥ
Вb
                                                                                                                                                                               Matches
                                                                                                                                                                                                       Query Match
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01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "comparative sequence analysis of cytokine genes from human and nonhuman primates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P48092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IL15_MACMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interleukin-15 precursor (IL-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submittee (JAN-1997) to the EMBL/GenBank/DDBJ databases.
1. FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
1. FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF IL-15
LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96003435; PubMed=7561102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003443;
pfam; PF02372; IL15;
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U19843; AAB60398.1; -
                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                              PROPER
                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                          Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunol. 155:3946-3954(1995).
121 ILSSNGNITESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                             121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                        61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISHESGDTDIHDTVENLIILANN 120
                                                                                      61 EDLIQSMHIDATLYTESDVHPSCKYTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WITH COMPONENTS OF IL-2R, GAMMA BUT NOT IL-2R ALPHA.
                                                                                                                                              1 MRISKPHLRSISIOCYLCLLLNSHFLTEAGIHYFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                   MRISKPHLRSVSIQCYLCLLLNSHFLTEAGIHVFILGCESAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                  AB000555
                                                                                                                                                                                 156
                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Signal
                                                                                                                                                                                                                                         162 AA;
                                                                                                                                                                                                                                                                                    30
49
83
90
127
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                       BAA19149.1;
                                                                                                                                                                                                                                             18194 MW;
                                                                                                                                                                                                 97.2%;
96.3%;
                                                                                                                                                                                                                                                                                                                                                                                                         Interleukin_15.
                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL).
K -> T.
I -> T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                 score 810; DB 1;
pred. No. 2.8e-67;
                                                                                                                                                                                                                                                                                                                                    INTERLEUKIN-15.
                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                              D233CF7FF6188C01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There are no
                                                                                                                                                                                                                   DB 1; Length 162;
                                                                                                                                                                                         Indels
                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                               0;
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AC
DT
                                                                  RESULT
                                                                                                                 Ъ
                                                                                                                                           Ŷ
                                                                                                                                                                           Db
                                                                                                                                                                                                      QУ
                                                                                                                                                                                                                                     Db
                                                     IL15_FELCA
                                                                                                                                                                                                                                                                 QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 156;
                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IL15_CERAE
30-MAY-2000 (Rel. 39, Created)
                        097687
                                 IL15_FELCA
                                                                                                  121 ILSSNGNITESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                            121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                     PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytokine; Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U03099; AAA18416.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grabstein K.H., Eisenman J., Shanebeck K., Rauch C., Srinivasan S., Fung V., Beers C., Richardson J., Schoenborn M.A., Ahdieh M., Johnson L., Alderson M.R., Watson J.D., Anderson D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR003443; Interleukin_15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
LYMPHOCYTES, STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning of a T cell growth factor that interacts with the beta chain of the interleukin-2 receptor.", Science 264:965-968(1994).
                                                                                                                                                                           61
                                                                                                                                                                                     61 EDLIQSMHIDATLYTESDYHPSCKYTAMKCFLLELQVISLESGDASIHDTYENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94233380; PubMed=8178155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 49-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithecinae; Cercopithecus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cercopithecus aethiops (Green monkey) (Grivet)
                                                                                                                                                                                                                    1 MRISKPHLRSISIQCYLCLLLKSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interleukin-15 precursor (IL-15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P40221
                                                                                                                                                                                                                                                 1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IL15_CERAE
                                                                                                                                                         EDLÍOSMHIDATLYTESDVHPSCKYTAMKCFLLELQVISHESGDTDIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAMMA BUT NOT IL-2R ALPHA
                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                      162 AA;
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                     30
49
83
90
127
                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IL15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                     18222 MW;
                                                                                                                                                                                                                                                                                                        96.6%;
96.3%;

    Mismatches

                                                                                                                                                                                                                                                                                                                  Score 805;
                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                            INTERLEUKIN-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                              1BF9A82644E1C9B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                    8e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 AA.
                                                                                                                                                                                                                                                                                                             DB 1; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                  0.
                                                                                                                                                                                                                                                                             Gaps
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Вр
                                                                                                                                                                                       IL15_PIG
                                                                                                                                                                                                                                                                        Qγ
                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                           IL15_PIG
Q95253;
                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Interleukin-15 precursor (IL-15).
SEQUENCE FROM N.A.
                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                          NCBI_TaxID=9823;
                                                                    Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                 121 GLSSNRNITETGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                            121 SLSSNGNVTESGCKECEELEEKNIKEFLOSFVHIVOMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003443; Interleukin_15.
Pfam; PF02372; IL15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               で大〇できて
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytokine; Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF108148; AAD05268.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barger A.B., Dean G.A., Lavoy A.S.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                     61 DKIIQSLHIDATLYTESDVHPNCKVTAMKCFLLELHVISLESKNETIHQTVENIIILANS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Lymph node;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutere
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                               61 EDLIQSMHIDATLYTESDYHPSCKYTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interleukin-15 precursor (IL-15).
                                                                                                                                                                                                                                                                                                                                             1 MRILKPYLRSTSIQCYLCLLLNSHFLTEACIPVFILSCINAGLPKTEANWQDVISDLKII 60
                                                                                                                                                                                                                                                                                                                                                                        1 MRISKPHLRSISIOCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                    134;
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49
83
90
104
127
                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18412 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                       82.8%; Score 690; DB 1; 82.7%; Pred. No. 2.6e-56;
                                                                                                                                                                                                                                                                                                                                                                                                          13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERLEUKIN-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              D8C7CEF7F40110DD CRC64;
                                                                                                                                                                 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ЬУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restrictions on
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                                                                                                                                                                                                                                                                                                                                                                                                    0;
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us-09-855-313a-4.rsp

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УŽ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ϋ́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вþ
                                                                                                                                                                                                                                                                                                                                                                                                       Дb
 RESULT 6
IL15_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97449311; PubMed=9305780; Canals A., Grimm D.R., Gasbarre L.C., Lunney J.K., Zarlenga D.S.; "Molecular cloning of cDNA encoding porcine interleukin-15."; Gene 195:337-339(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003443; Interleukin_15.
pfam; pF02372; IL15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytokine; Glycoprotein; Signal
                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                 028028;
               modulation of transcription by exogenous stimulation.";
J. Interferon Cytokine Res. 17:473-480(1997).
-!- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF
                                                         Canals A., Gasbarre L.C., Boyd P.C., Almeria S., Zarlenga D.S.; "Cloning and expression of bovine interleukin-15: analysis and
                                                                                                                                                                                                                      Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                       121 SLSSIEYKTESGCKECEELEEKNINEFLKSFIHIVOMFINDS 162
                                                                                           MEDLINE=97426124; PubMed=9282828;
                                                                                                             STRAIN-Holstein;
                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                        Bovidae; Bovinae; Bos.
                                                                                                                                                                                      Mammalia;
                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                  Interleukin-15 precursor (IL-15).
                                                                                                                                                                                                                                                                                                                                                                                                                                  121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                       NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 EDLIRSTHMDATLYTESDAHPNCKVTAMKCFLLELRVILQESRNSDISDTVENLIILANS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15 WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2RALPHA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRILKPCLRSTCIQCYLCLLLNSHELTEDGIHVFILGCISAGLPKTEATWQHVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE IL-15 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRISKPHLRSISIOCYLCLLLNSHFLTEAGIHVFILGCESAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U58142; AAB72031.1;
LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
                                                                                                                                                                                                                                                                                                                                BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                      Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18437 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.5%;
                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 662;
pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (F; 7EF7992391883446 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                       162 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytokine; Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U42433; AAA85130.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHEEP
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                                                                                                  J. Interferon Cytokine Res. 0:0-0(1999).

-i- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
-i- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERACTION OF IL-15
-IXMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-12
-WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
GAMMA BUT NOT IL-2R. ALPHA (BY SIMILARITY)
                                                                                                                                                                                                                                                                    Casey G.J., Chaplin P.J.; "Isolation of interleuring name Tank Transcripts from T and B
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ovis aries (Sheep).
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This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                            circulating in efferent lymph.";
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
                                              -!- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
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                                                                                   SUBCELLULAR LOCATION:
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2372; IL15; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metazoa; Chordata;
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104
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N-LINKED (GLCNAC...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                            "Chromosomal assignment and genomic structure of IL15.", Genomics 25:701.706(1995).
                                                                                                                                                                                                                                             Anderson D.M., Johnson L., Glaccum M.B., Copeland N.G., Gilbert D.J. Jenkins N.A., Valentine V., Kirstein M.N., Shapiro D.N., Morris S.W. molecular K., Cosman D.;
                                                                                                                                                                                                                                                                                           STRAIN-WC/REJ x C57BL/6J; TISSUE=Bone marrow; MEDLINE=95278940; PubMed=7759105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                   Anderson D.M.,
                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Interleukin-15 precursor (IL-15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P48346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 EHLIQSMHMDATLYTESDAHPNCKVTALQCFLLELRVILHESKNAAIYEIIENLTMLADR 120
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                                                                                                                    SIMILARITY: BELONGS TO THE IL-15 FAMILY.
                                                                                                                                                                             FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRILKPYLRSTSIQCYLCLLLNSHFLTEAGIHVFILGCISAGLPKTEANWQSVIHDLKTI 60
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                                                                                                                                     SUBCELLULAR LOCATION: Secreted
                                                                                                                                               WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R GAMMA BUT NOT IL-2R ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi;
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 650;
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N-LINKED (GLCNAC. ..) (POTENTIAL)
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                  Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).
                                                                                                           -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
                                                                                                                                                                                                                                        STRAIN=Wistar; TISSUE=Spleen;
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (LONG AND SHORT FORMS).
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P97604: 054847;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                   Gastroenterology 111:1706-1713(1996).
                                                                                                                                                                                                                                                                                                                                              MEDLINE=97098212: PubMed=8942753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAT
                                                                                                                                                                                                                                                                                                                                      Reinecker H.C.,
                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Sprague-Dawley;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (LONG FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interleukin-15 precursor (IL-15).
                                                                                                                                                                                                                                                                                                       Intestinal epithelial cells both express and respond to interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L15_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TLSSNKNVAESGCKECEELEEKTFTEFLOSFIRIVOMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SLSSNGNVTESGCKECEELEEKNIKEFLOSFVHIVOMFINTS 162
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                                                                                                                                                                                                                                                                                                                                                          TISSUE=Jejunum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                          "Vickers M.F., Yao S.Y., Baldwin S.A., Young J.D., Cass C.E.;
"Nucleoside transporter proteins of Saccharomyces cerevisiae.
"Nucleoside transporter (FUI1) with high uridine selectivity Demonstration of a transporter (FUI1) with high uridine selectivity in plasma membranes and a transporter (FUN26) with broad nucleoside selectivity in intracellular membranes.";
J. Biol. Chem. 275:25931-25938 (2000).
J. BIOL. Chem. 275:25931-25938 (2000).
CYTIDINE) AND MOST LIKELY FUNCTIONS TO TRANSPORT NUCLEOSIDES CYTIDINE) AND MOST LIKELY FUNCTIONS TO TRANSPORT NUCLEOSIDES
                                                                                                                                                                                                                           MEDLINE-3320532; PubMed-8458570; Ouellette B.F.F., Clark M.W., Keng T., Storms R.K., Zhong W.W., Ouellette B.F.F., Clark M.W., Keng T., Storms R.K., Zhong W.W., Zeng B., Fortin N., Delaney S., Barton A.B., Kaback D.B., Bussey H.; Zeng B., Fortin N., Delaney S., Barton A.B., Kaback D.B., Bussey H.; Senguencing of chromosome I from Saccharomyces cerevisiae: analysis "Sequencing of chromosome I from Saccharomyces cerevisiae: analysis of a 32 kb region between the LTE1 and SP07 genes.";
                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                        FUN26 OR YAL022C
                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleoside transporter FUN26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P31381;
01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TLSSNKNVIESGCKECEELEERNFTEFLQSFIHIVQMFINTS 162
                                                                                                                                                                                                                                                                                                              STRAIN-S288C
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                        Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                         MEDLINE=20408929; pubMed=10827169;
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS 162
                                                                                                                                                                                 CHARACTERIZATION.
                                                                                                                                                                                                               Genome 36:32-42(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKILKPYMRNTSILYYLCFLLNSHFLTEAGIHVFILGCVSVGLPKTEANWIDVRYDLEKI 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YEAST
SUBCELLULAR LOCATION: Integral membrane protein (Potential)
               ACROSS INTRACELLULAR MEMBRANES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 AA;
                                                                                                                                                                                                                                                                                                                                                                                        Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30
49
83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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108
119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.1%;
72.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal; Alternative splicing.
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pred. No. 1.2e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. ..) (POT MISSING (IN SHORT ISOFORM); DA68097A83065AEA CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERLEUKIN-15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            517 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
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     REB1_KLULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L05146; AAC04935.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
TRANSMEM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01733; Nucleoside_tran; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S36712; S36712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
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                    Morrow B.E., Ju Q., Warner J.R.;

"A bipartite DNA-binding domain in yeast Reblp.";

Mol. Cell. Biol. 13:1173-1182(1993),

Mol. Cell. Biol. 13:1173-1182(1993),

Mol. Cell. Biol. 13:1173-1182(1993),

HOLTON: DNA-BINDING PROTEIN THAT RECOGNIZES SITES WITHIN BOTH

-1- FUNCTION: DNA-BINDING PROTEIN THAT RECOGNIZES SITES WITHIN BOTH

1-- FUNCTION: DNA-BINDING PROTEIN THAT RECOGNIZES WITHIN BOTH

1-- FUNCTION: DNA-BINDING PROTEIN THAT RECOGNIZES WITHIN BOTH

1-- FUNCTION: AS WITHIN BOTH

                                                                                                                                                                                                                                                                                                                                        Kiuyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q05950;
                                                                                                                                                                                                                                                                                                            Saccharomycetales; Saccharomycetaceae; Kluyveromyces
                                                                                                                                                                                                                                                                                                                                                                                                              DNA-binding protein REB1 (QBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REB1_KLULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  461 TNGHVISMSFMKVPEQLDNDDEKEAAGGFTNI---FVST 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403 DQKFTPRKTFIYSLLRVAAIPLFLMFTAITSSSSGDEEHNGSV--IVDLCYMLLQFLFGV 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 YLVLSIFTTFVVTLVFPVFASATYVTGLPLSNAQYIPLIFTLMNLGDLYGRVIADWPMFR 402
                                                                                                                                                                                                                    MEDLINE=93140755; PubMed=8423784;
                                                                                                                                                                                                                                                                                          NCBI_TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 SNGNV-TESGCKECEELEEKNIKEFLQSFVHIVQMFINT 161
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 YLCLLLNSHFLTEAGIHVEILGCFSAGLPKTEANWVNVISDLKKIEDLIQSMHIDATLYT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 ESDVHPS-----CKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS----- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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(WHERE R IS ANY PURINE) (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    517 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 40, Last annotation update)
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171
194
234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.4%;
25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               595 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                    -!- FUNCTION: HYDROLYTIC DEAMINATION OF THE S-TRIAZINE SUBSTRATE
                                                                                                                                                                                                  strains capable of dealkylating and dechlorinating the herbicide
                                                                                                                                                                                                                "Cloning and expression of the s-triazine hydrolase gene (trzA) from Rhodococcus corallinus and development of Rhodococcus recombinant
                                                                                                                                                                                                                                                                        MEDLINE=96011356; PubMed=7592318;
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=36822;
                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae.
                                                                                                                                                                                                                                                                                                                                                                                                              S-triazine hydrolase (EC 3.8.1.-) (N-ethylammeline chlorohydrolase)
                                                                                                                                                                                                                                                                                                                                                 Actinomycetales; Corynebacterineae; Gordoniaceae; Gordonia.
                                                                                                                                                                                                                                                                                                                                                                                            Rhodococcus corallinus
                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRZA_RHOCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00037; MYB_1; 2.
PROSITE; PS00334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 NDDQQDDVSNLIQEAAAKASHIINPATQSNGKSFDESEEEALEQFIKEYQKI 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 DASIHDTVENLIILANNSLSSNGN-VTESGCKECEELEEKNIKEFLQSFVHI 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 PKKEKSEERSYGDLSNIDDHVDDVSVSGSIPSQVRLKKTAEVLP-----KVLSSESH 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear protein; DNA-binding; Transcription regulation; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00249; myb_DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A48077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
                                                                                                                                                                           Bacteriol. 177:5748-5755(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 PKTEANWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESG 103
                                                                                                     PATHWAY: Melamine degradation pathway; first step. SIMILARITY: BELONGS TO THE ATZ/TRZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P06876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L03789; AAA61343.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28;
                                                                                                                                                                                                                                                    Seffens W., Mulbry W., Behki R.M.;
                                                                                                                                                                                                                                                                                           15444R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001005; Myb_DNA_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      595 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SANT; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68050 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.0%; Score 83.5;
25.0%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYB 1.
MYB 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6A85334CB3AF8162 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9;
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRPA_BUCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                SEQUENCE
                                                                                    TIGREAMS; TIGR00262; trpA; 1.
PROSITE: PS00167; TRP_SYNTHASE_ALPHA; 1.
                                                                                                                      InterPro; IPR003009; FMN_enzyme.
InterPro; IPR002028; Trp_synthaseA.
Pfam; PF00290; trp_syntA; 1.
ProDom; PD001535; Trp_synthaseA; 1.
                                                                                                                                                                                                      EMBL; U09185; AAA92797.1; - HSSP; P00929; 2WSY.
                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                          Tryptophan biosynthesis; Lyase
                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE TRPA FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endosymbiont (Buchnera) of the aphid Schlechtendalia chinensis.";
Insect Mol. Biol. 4:47-59(1995).
-!- FUNCTION: THE ALPHA SUBUNIT IS RESPONSIBLE FOR THE ALDOL CLEAVAGE
OF INDOLEGLYCEROL PHOSPHATE TO INDOLE AND GLYCERALDEHYDE 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=95261545; PubMed=7742976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buchnera aphidicola (subsp. Schlechtendalia chinensis).
Bacteria: Proteobacteria: gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tryptophan synthase alpha chain (EC 4.2.1.20).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genetics of the tryptophan biosynthetic pathway of the prokaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=118110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRPA_BUCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380 IGSLEAGKRADIITLDLRHAQTTPAHDLAATIVFQAYGNEVNDVLVNGSV 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 TVGIGTDDANCNDSVNLISDMKVLALIHRAAHRDASIITPEKIIEMATIDGARCIGMADQ 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01685; ATZ_TRZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L16534; AAA90931.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 VISLESGDAS-----IHDTVENLIILAN----NSLSSNGNV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 SAGLPKTEANW----VNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                 E-tryptophan + glyceraldehyde 3-phosphaté + H(2)0.
PATHMAY: Tryptophan biosynthesis; fifth (last) step.
SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.-Y., Baumann P., Moran N.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002604; ATZ_TRZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                      30301 MW;
  9.7%;
25.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50727 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.9%; Score 82.5;
23.6%; Pred. No. 3
Pred. No. 2.3;
                  Score 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                  7879A03A5C7A50AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64D953DB2E92C73E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 41; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 AA
                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 476;
              Length 269;
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Qy D. QΥ

43

456 AA.

Murinae; Rattus.

Matches

g

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RESULT 14

_BUCAI

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Matches
                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Exodeoxyribonuclease V gamma chain (EC 3.1.11.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Tokyo 1998;
MEDLINE-20445173; PubMed-10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EX5C_BUCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buchnera sp. APS.";

Nature 407:81-86(2000).

-i- FUNCTION: EXHIBITS A WIDE VARIETY OF CATALYTIC ACTIVITIES

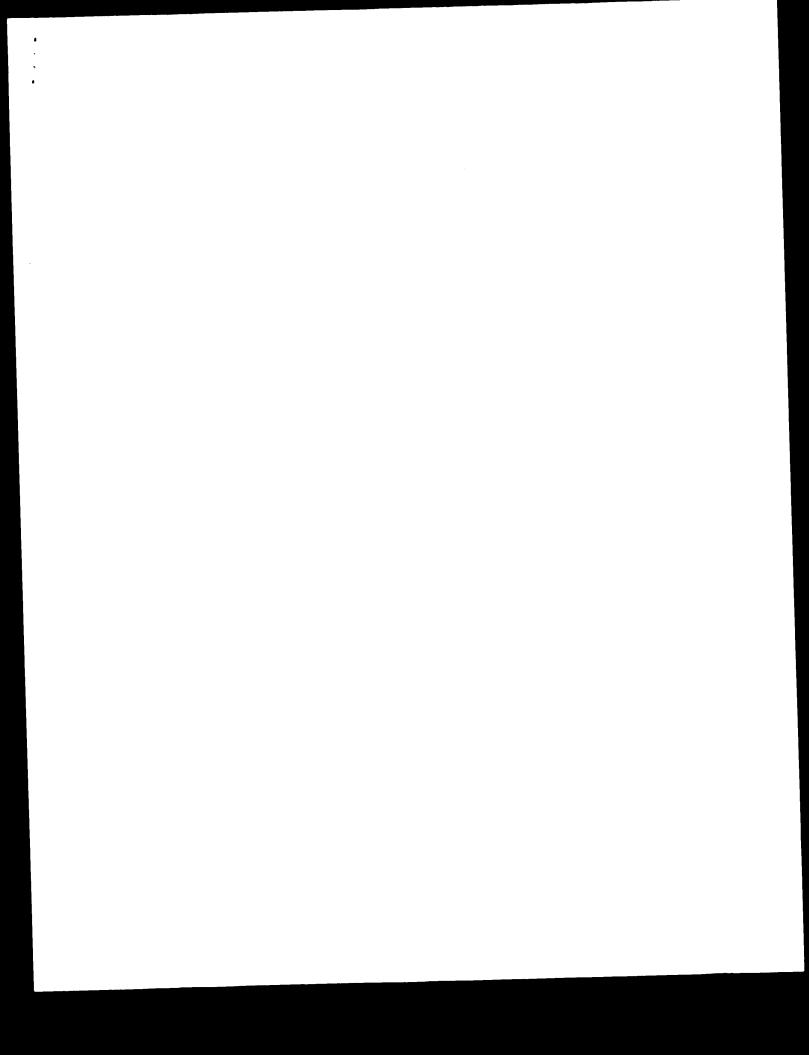
-i- FUNCTION: EXP-DEPENDENT EXONUCLEASE, ATP-STIMULATED ENDONUCLEASE, ATP-DEPENDENT HELICASE AND DNA-DEPENDENT ATPASE ACTIVITIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Buchnera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            symbiotic bacterium).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 STGYIYLLS-RSGVTGTDKKIIVPSLNLIKNLKKITE 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 DSVLIADLPVEESN-----DFRKCAIANNISSVFVCP------HDAKKNVIKKISLY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 IQKAHLRAFSSKMNIYLCFEMLQKIRKKYNTIPIGLLLYANLIFKFGINNFYLKCFNVGI 123
                                                                                                                                                                                                                                                                                                        Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase; DNA repair;
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                          EMBL; AP001119; BAB13151.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  579 LSSNYLKKISINILKKIFFYKYYDNNHEIFLPGVVNFCYPDSVCYIPFKVICMIGTDHTS 638
                                              639 IPKT--NYLDNENLLKKYPLIGDINLYQKYSYLEVQSLSCAEKYFYISYIGYSVKDESKV 696
            80 HPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGN---VTESGCKEC 136
                                                                                  43 LPKTEANWVNVISDLKK---IEDL------IQSM------HIDATLYTESDV 79
                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----LPKTEANWVNVISDLKK--IEDLIQSMHIDATLYTESDVHPSCKVTAMKCFIL 93
                                                                                                                                                          3 ISKPHLRSISIQCYLCLLL-----NSHFLTEAGIHVF------ILGCFSAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: Exonucleolytic cleavage (in the presence of ATP) in either 5'- to 3'-or 3'- to 5'-direction to yield 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELQVISLESGDASIHDTVENLIILANNSLSSNGNVTE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: CONSIST OF THREE SUBUNITS; RECB, RECC AND RECD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphooligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY)
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                                                                                                                                                                                                                                                                        1070 AA; 128578 MW;
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                    9.7%; Score 80.5; DB 1; Length 1070; 23.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Mismatches
                                                                                                                                                                                                        32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                              8F644C84877981AF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
                                                                                                                                                                                                              69;
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                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
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                                                                                                                                                                                                                    필필증
                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawanomoto M., Motojima K., Sasaki M., Hattori H., Goto S.; "cDNA cloning and sequence of rat ribonuclease inhibitor, and tissue distribution of the mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P2931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochim. Biophys. Acta 1129:335-338(1992).
-i. FUNCTION: INHIBITOR OF PANCREATIC RNASE AND ANGIOGENIN. MAY ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92162755; PubMed=1536887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribonuclease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RINI_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      739 KKOFFYETKNIESFIQ 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 EE---LEEKNIKEFLO 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              697 HPSILVDQL-----LNYITL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the DMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: BRAIN, HEART, LUNG, LIVER, SPLEEN, TESTES AND KIDNEY: HIGHEST IN THE LUNG AND LOWEST IN THE HEART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: CONTAINS 15 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00370; LRR; 12
SMART; SM00368; LRR_RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S20597; S20597
HSSP; P10775; 2BNH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X62528; CAA44388.1;
                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00560; LRR; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001611; LRR
                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003590; LRR_RNinh.
                                                                        SEQUENCE
                                                                                                                                                REPEAT
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                                                                                                                                                                                                                                                                                                                                                                          Leucine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR003592; LRR_out.
                                                                        414
456 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                            128
157
185
                                                                            49905 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                12.
                                                                                                                                                                                                                                                                                                                                                                          repeat.
                      9.5%; Score 79; DB 26.1%; Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                  LRR
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                                                                                                                                                                                                                                                                                  LRR
                                                                                                                                                                                                                                                                                                  LRR
                                          Score 79;
                                                                                                LRR
                                                                                                                                                      LRR
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                                                                                                                  LRR
                                                                                                                                    LRR
                                                                            8518E5B1F09E5998 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----NFCFIGDQNLSYKENSKKITKYLCKKH 738
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Ş Дb Qy д Š

В4

DB 1; Length 456;

Searc Job t	Db	Оy	Db	Qy	Db	Ϋ́	ма
Search completed: February 20, 2003, 16:29:05 Job time : 17.5 secs	270 DLCRVLRAKQSLKE 283	135 E-CEELEEK-NIKE 146	211 CKDLCDVVASKASLQELDLGSNKLGNTGTAALCSGL-LLPSCRLRTLWLWDCDVTAEGCK 269	79 VHPSCKVTAMKCFLLELQVISLESGDASIHDTVENITTLANNSTSS	170 LVLSNNDFHEAGIHTLCQG	19 LLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKIEDLIOSMHIDATIVTESS 70	Matches 35; Conservative 22; Mismatches 51; Indels 26; Gaps 5;



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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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sp_mhc:*
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sp_archeap:*
                sp_bacteriap:*
                               sp_rvirus:*
                                             sp_unclassified:*
                                                                                    sp_virus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

12 14 15	11 11 11 11	Result No.
88.5 88 88 88 87.5	533 257 248 117.5 116.5 116.5 111.5 111.5 111.5 117.5 99.5	Score
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16 Q92GE/ 16 Q82PC3 12 Q9YW85 17 Q9YW85 18 Q8Y89 18 Q8W9S7	0	SUMMARIES
092ge7 rickettsi 08xpc3 clostridium 09xw85 melanoplus 09xw85 clostridium 08xn89 clostridium 061493 drosophila 08w9s7 mesostigma	OBspyO canis famil Obdev5 gallus gall Obdev5 gallus gall ObjeT5 meleagris g ObjeT7 meleagris g ObjeT8 gallus gall O7888 gallus gall O4236 gallus gall O4236 gallus gall O90bbe4 homo senis	Description

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СЭУКИ1 numan immun		2 Zea mavs	0	Q9pib4 campylobact	Vydja/ shewanella	Source citetillocode		085479 zea mave (m	002497 drosophila	Caroza pactitus ha	Transaction Til	09007/ 6	Zea mave	016199 caenorhabdi	V93YUI arabidopsis		021697 02000t-13:	091m15 lumpy skin	Zea mave /	0//384 plasmodium	Q91K12 human immun			illacaca	i indition		O9atd8 gossynium	Q8reu9 fusobacteri		0	CACAGE anabaena sp	7	

ALIGNMENTS

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                                                                                                                                                                                  Matches 102;
                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

A stang 2. Byrne K.M., Michal J.;

"Cytokine expression in muscle satellite cells of canine.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

SEMBL; AF479882; AAL87133.1; -.

NON_TER 128 128 128

SEQUENCE 128 AA; 14192 MW; FC6BC2C2EB1765934 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21 Created)
01-JUN-2002 (TrEMBLrel. 21 Last sequence update)
01-JUN-2002 (TrEMBLrel. 21 Last annotation update)
1. Interleukin 15 (Fragment).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
121 DLSSKGNI 128
                            121 SLSSNGNV 128
                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8SPY0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08SPY0
                                           61 DNLIQCIHMDTTLYTESDVHPSCKITAMKCFLLELGVISLESGSHPIKEAVENLIILANS 120
                                                            1 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCESAGLPKTEANWVNVISDLKKI 60
                                                                                                      1 MRISKPHLRSTCIQCYLCLLLNSHFLTEAGIHVFILGCINAGLPKTEANWQDVILDLEKI 60
                                                                                                                                                                                            Local Similarity
                                                                                                                                                                     64.0%; Score 533; DB 6; Length 128; 79.7%; Pred. No. 2.1e-45; Conservative 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 AA.
                                                                                                                                                                 0; Gaps
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0

46; Indels

38; Gaps

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Q9DEV5
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                  Q9W756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq-
01-DEC-2001 (TrEMBLrel. 19, Last annum trepleukin 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9DEV5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9DEV5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stepaniak J.A., Kolodsick J.E., Hu W., Sundick R.S.; "Chicken interleukin 15 precursor, allelic variant."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AY005476; AAG02253.1; ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
Interleukin-15 precursor (Interleukin 15 precursor).
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                       Q9W756;
                                                                                                                                                                                                                                                                                                                                                                                       Q9W756
                                                                                                                                                                          STRAIN=SCWL; TISSUE=LIVER;
Burnside J., Sofer L.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken)
                                                                                     Choi K.D., Lillehoj H.S., Burnside J.; "Gallus gallus mRNA for IL-15 precursor "; submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 IL-----KNGNARFATYQLNSTTSKKCKECEEYEEKNFTEFIQSFVKVIQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 LITLANNSLSSNGN------VTESGCKECEELEEKNIKEFLOSFVHIVO 156
                                                             EMBL; AF152927; AAD38392.1; EMBL; AF139097; AAF61446.1;
                                                                                                                               STRAIN=SC; TISSUE=LIVER;
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 ELIK---TSEDIDVSLYTANTYEDIECQEPVMRCFFLEMKVILHECGIKKCSRKHD-VWN 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 KTHYKSICLQYQLYLLINSHFFCLLKNKTGLTIFFL---CAYYPKTEANHCKWSDYLKDL 78
                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Loca t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 KPHLRSISIQCYLCLLLNSHFL----TEAGIHVFILGCFSAGLPKTEAN---WVNVISDL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKIEDLIQSMHIDATLYTESDVHP-SCKVTAMKCFLLELQVISLESGDASI---HDTVEN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69;
                   PF02372; 1L1:
NCE 187 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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2372; IL15; 1.
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                                                  IPR003443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                    IL15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21879 MW; B701CFCC7431B658 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.9%; Score 257; DB 1
39.9%; Pred. No. 1e-17;
                                                  Interleukin_15.
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Last annotation update)
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Length 187;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interleukin-2 precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Turkey and chicken interleukin-2 cross-react in in vitro proliferation assays despite limited amino acid sequence identity."; J. Interferon Cytokine Res. 20:161-170(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20177011; PubMed=10714551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ007463; CAB65230.1; ...
InterPro; IPR000779; Interleukin-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lawson S.A., Rothwell L., Kaiser P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 KTHVKSICLQYQLYLLLNSHFFCLLKNKTGLTIFFL---CAYVPKTEANHCKWSDVLKDL 78
                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 KPHLRSISIOCYLCLLLNSHFL----TEAGIHYFILGCFSAGLPKTEAN---WVNVISDL 57
                                                                                                                                                                                                                                                         Q9IAC7
Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris
                              Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                          Q9IAC7;
                                                                                                                                                                                                                                                                                                                                                                                                                122 NDKKNFPDFLQQLTNFVR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 LEEKNIKEFLQSFVHIVQ 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 VFILGCFSAGLPKTEANWVN------VISDLKKIEDLIQSMHIDATLYTESDVHP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 VLIFSCISVALLMTTAYGASLSPEKLEILPALIKDLEILEESKNKIHV--VLYTPNEI-K 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELIK---TSEDIDVSLYTANTYEDIECQEPVMRCFFLEMKVI-LHECDIKKCSRKHDV-- 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECSQQTLQCYLEEMVMLKKETEDEPETKNEFKNALQN1KKNLHRLKDLSPTGGECKICEA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCKVTANKCFLLELQVISLESGD-ASIHDTVENLIILANNSLSSNGNVTESG--CKECEE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00189; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR003443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 AA; 16511 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.1%; Score 117.5; DB 1
25.4%; Pred. No. 0.00056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interleukin_15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29; Mismatches
                                                                                                                                            Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERLEUKIN-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1A5DE8E7D49E5CCB CRC64;
                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 AA.
                                                                                                                                                                                                                                                                          143 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 17; Gaps
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5.

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Qy
                                            Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
042288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ωy
                                                                                            Matches
                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
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RN
RP
RA
RT
DR
DR
DR
                                                                                                                                                                                                                                                                                              STRAIN-KESTREL LEGHORN; TISSUE-SPLEEN;
Hutchins J.E., Tyczkowski J.K., Poston R.M., Hester J.B.,
Girardi R.S., Liu H., Doelling V.W., Ricks C.A., Bland M.M.,
"Gallus gallus mRNA for IL-2 precursor.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                  SEQUENCE
                                                                                                                                                                             VARIANT
                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                               EMBL; AF033563; AAB87502.1; InterPro, IPR000779; Interleukin-2. InterPro; IPR003443; Interleukin_15.
                                                                                                                                                                 VARIANT
                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                            SMART; SM00189;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken)
82 SCKVTAMKCFLLELQVISLESGDASIHDT-VENLIILANNSLSSN-----GNVTESGCK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interleukin-2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                042288
                                                   33 VFILGCFSAGLPKTEA------NW----VNVISDLKKIEDLIQSMHIDATLYTESDVHP 81
                          5 VLIFGCISVAMLMTTAYGASLSSEKWKTLQTLIKDLEILENIKNKIHLE--LYTPTETQ- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 NDKKNFPDFLQQLTNLLR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases EMBL: AF209705; AAF33206.1; ... InterPro; IPR000779; Interleukin-2.
                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 LEEKNIKEFLQSFVHIVQ 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02372; IL15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003443; Interleukin_15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Romero C.H., Cai X.Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Turkey interleukin-2 gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 ECSQQTLQCYLEEMVMLKKEIEDEPEIKNEFKNALQNIKKNLHRLKDLSPTGGECKICEA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 SCKVTAMKCFLLELQVISLESGD-ASIHDTVENLIILANNSLSSNGNVTESG--CKECEE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 VFILGCESAGLPKTEANWVN------VISDLKKIEDLIQSMHIDATLYTESDVHP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 VLIFSCISVALLMTTAYGASLSPEKLETLPALIKDLETLEESKNKTHV--VLYTPNET-K 61
                                                                                             37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00189;
                                                                                         Conservative
                                                                                                                                                143 AA;
                                                                                                                                                                23
28
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                         IL15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IL2;
                                                                                                                                                                                      143
28
                                                                                                                                             16429 MW;
                                                                                   14.0%; Score 116.5; DB
26.1%; Pred. No. 0.0007;
tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16442 MW; 1A4AD959348BB22B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.0%; Score 116.5; DB 24.6%; Pred. No. 0.0007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Mismatches
                                                                                                                                                                                     E -> A
                                                                                                                                                                                               INTERLEUKIN-2.
                                                                                                                                                                                                               POTENTIAL
                                                                                                                                        7DCDFEACBD48F5AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 AA.
                                                                                                            DB 13; Length 143;
                                                                              54; Indels 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56; Indels 17; Gaps
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RESULT 8
                                                                                               В
                                                                                                                           Ş
                                                                                                                                                                                       Qγ
                                042396
                                                                                                                                                            В
                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                    Qγ
                                                                                                                                                                                                                                                                                                                                                  RA RA
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             073883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
042396;
042396;
                                                                                     118 ICEANNKKKFPDFLHELTNFVR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yu L., Li J.R., Huang Y.W., Meng S.S.; "Cloning and sequence analysis of a Chinese local chicken IL-2 gene."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ24516; CAA12025.1; "MENT APRITAGES AND CACA".";
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                    135 ECEELEEKNIKEFLQSFVHIVQ 156
                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00189; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL: AF017645; AAC96064.1; EMBL; AY029588; AAK37775.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Choi K.D., Lillehoj H.S., Song K.D., Han J.Y.; "Molecular and Functional Studies of Chicken IL-15 Which Promotes the Growth of gamma/delta TCR T Lymphocytes: Phenotypic and Functional Characterization of IL-15 dependent gamma/delta T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003443; Interleukin_15.
Pfam; PF02372; IL15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000779; Interleukin-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                         62 ECTOOTLOCYLGEVVTLKKETED----DTEIKEEFVTAIONIEKNLKSLTGLNHTGSECK 117
                                                                                                                                                                                                                                   33 VFILGCESAGLPKTEANWVN------VISDLKKIEDLIQSMHIDATLYTESDVHP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FISSUE=SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dev. Comp. Immunol. 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-EBC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           073883
073883;
                                                                                                                                                                      82 SCKVTAMKCFLLELQVISLESGDASIHDT-VENLIILANNSLSSN------GNVTESGCK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaiser P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IL-2 precursor (Inte: INTERLEUKIN-2 OR IL2
                                                                                                                                                                                                     5 VLIFGCISVAMLMTTAYGASLSSAKRKPLQTLIKDLETLENIKNKIHLE--LYTPTETQ- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 ICEANNKKKFPDFLHELTNFVR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 ECEELEEKNIKEFLOSFVHIVO 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 ECTOQTLOCYLGEVVTLKKETED----DTEIKEEFVTAIQNIEKNLKSLTGLNHTGSECK 117
                                                                                                                                                                                                                                                                                   36;
                                                                                                                                                                                                                                                                                                                                    143 AA; 16337 MW; B1BCFEA97A54846F CRC64;
        PRELIMINARY;
                                                                                                                                                                                                                                                                       Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mariani P.;
                                                                                                                                                                                                                                                                                                                                                                  23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Interleukin-2).
                                                                                                                                                                                                                                                                                                                                                              143
                                                                                                                                                                                                                                                                                   13.7%; Score 114.5; DB 13; Length 143; 25.4%; Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                              22
        PRT;
                                                                                                                                                                                                                                                                                                                                                         INTERLEUKIN-2
                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
      143 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 AA
                                                                                                                                                                                                                                                                    54; Indels
                                                                                                                                                                                                                                                                    25; Gaps
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

Interleukin-2.

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Q9DDN9
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                                                                                         da
       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                               Query Match
                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sundick R.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=OBESE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02372; IL15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000779; Interleukin-2.
InterPro; IPR003443; Interleukin_15.
                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                            Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris
                                                                                                                                                                                                                                                                                                          Meleagris gallopavo (Common turkey).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                             Q9DDN9
                                                                                                                                              EMBL, AF308569; AAG35189.1;
InterPro; IPR000779; Interleukin-2.
InterPro; IPR003443; Interleukin-15
                                                                                                                                                                                                         Hu W., Kolodsick J.E., Stepaniak J.A., Sundick R.S.; "Turkey interleukin-2.";
                                                                                                                                                                                                                                                                                                                                         Interleukin-2 (Fragment)
                                                                                                                                                                                         Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                         TISSUE-SPLEEN;
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                NCBI_TaxID=9103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 ICEANNKKKFPDFLHELTNEVR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 ECEELEEKNIKEFLQSFVHIVQ 156
                                                                                           SEQUENCE
                                                                                                                                      Pfam; PF02372; IL15;
                                                                                                            NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 VFILGCFSAGLPKTEANWVN------VISDLKKIEDLIQSMHIDATLYTESDVHP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 ECTQQTLQCYLGEVVTLKKETED----DTEIKEEFVTAIQNIEKNLKSLTGLNHTGSECK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 SCKVTAMKCFLLELQVISLESGDASIHDT-VENLIILANNSLSSN-----GNVTESGCK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cloned chicken lymphokine homologous to both mammalian IL-2 and IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunol. 0:0-0(1997)
      38 CFSAGLPKTEANWVN------VISDLKKIEDLIQSMHIDATLYTESDVHPSCKVT 86
                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLIFGCISVATLMTTAYGASLSSAKRKPLQTLIKDLEILENIKNKIHLE--LYTPTETQ- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF000631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00189;
                                        32;
                                                                                                                     SM00189; IL2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 AA; 16307 MW; B9B1E9997A54935F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                            135 AA; 15460 MW; 326F88A3563D13E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                      Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gill-Dixon C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB63150.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.4%; Score 111.5; DB 13; Lewy...
25.4%; Pred. No. 0.0022;
wismatches 55; Indels
                                                      12.9%; Score 107.5;
24.1%; Pred. No. 0.0
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                                                                                                                                                                                                                                                                                                                                                                                                                  135 AA.
                                                          0.0051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13; Length 143;
                                                                       DB 13; Length 135;
                                            54; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
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RESULT 10
Q9HBE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QУ
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                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                   Q92GE7
                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20531754; PubMed=11081504;

MEDLINE-20531754; PubMed=11081504;

Parrish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C.,

Parrish-Novak J., Dillon S.R., Nelson A., Hest J., Schrader S.,

Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,

Burkhead S., Heipel M., Brandt C., Kuijper J.L., Kramer J.,

Conklin D., Presnell S.R., Berry J., Shiota F., Bort S., Hambly K.,

Conklin D., Presnell S.R., Berry J., Shiota F., Cotton-Day C., Gilbert T.,

Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,

Rayond F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,

Maurer M., Kaushansky K., Holly R.D., Foster D.;

Maurer M., Kaushansky K., Holly R.D., Foster D.;

Maurer M., Kaushansky K., Holly R.D., Foster D.;

Maurer M., Kaushansky K., Holly R.D., Foster D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9HBE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9HBE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interleukin 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 FPDFLQQLTNLLR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 IKEFLQSFVHIVQ 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulation of lymphocyte function."; Nature 408:57-63(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 TLQCYLEEMVMLEKEIEDEPEIKNEFKNALQNIKKNLHRLKGLSPTGGECKICEANDKKN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 AMKCFILELQVISLESGD-ASIHDTVENLIILANNSLSSNGNVTESG--CKECEELEEKN 143
                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                      Q92GE7
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
                                                                                                                                                                                                                                                                                                               Q92GE7;
                                                                             SEQUENCE FROM N.A. STRAIN=MALISH 7;
                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
                                                                                                                                                                                              Rickettsia conorii
                                                                                                                                                                                                                                  Hypothetical protein RC1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 TVENLII--LANNSLSSNGNVTES----GCKECEELEEKNIKEFLQSFVHIVQMFIN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CISVALLMTTAYGASLSPEKLEILPALIKDLEILEESKNKIHV--VLYTPNEI-KECSQQ 58
                                                        MEDLINE=21442074; PubMed=11557893;
                                                                                                                                      NCBI_TaxID=781;
                                                                                                                                                        Rickettsiaceae; Rickettsieae; Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                              94 RIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 IDTVDQLKNYVNDLVPEF-----LPAPEDVETNCEWSAFSCF----QKAQLKSANTGNNE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 VNVISDLKK-1EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF254069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG29348.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18652 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.9%; score 99.5;
25.9%; Pred. No. 0
                                         Renesto-Audiffren P., Fournier P.-E., Barbe V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54EFD4EED3AB97FE CRC64;
                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 AA
                                                                                                                                                                                                                                                                                                                                               433 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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5

SQ RAT

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RESULT 13
                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8XPC3
                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
                                                    09YW85
                                                                                                                  130 MKNSHD-----EETIKSNAKIFVES 149
                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Complete SEQUENCE 167 AA; 18821 MW;
                                                                                                                                                 125 NGNVTESGCKECEELEEKNIKEFLQS 150
                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=13 / TYPE /
                                                                                                                                                                 70 RTYSETGKLNNTMIEGLERSNNFFKCLIEDLKGVKVPEKFASYNDDIINNLNKAKTSLEA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridiales; Clostridiaceae; Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                               77 SDVHPSCKV-----TAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSS 124
                                                                                                                                                                                                                               14 LSLEVLGCSTSG----EKNTINIPIEKSREEEKSKDEEEYIDKISSTIVNMSVDGSIKNM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=11792842;
                                                                                                                                                                                                                                                             31 IHVEILGCFSAGLPKTEANWVNVISD-------LKKIEDLIQSMHIDATLYTE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein CPE0042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QBXPC3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8XPC3
                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 PRESFINT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 GTASI----LSQLYKVMNDYIFSQGNITETSGADFLGLNECTKEEAMSALQNYNAYTETLI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 GDASIHDTVENLIILANNSLSSNGNVTES-----GCKECEELEEKNIKEFLQSFVHIV- 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein; Complete proteome.
SEQUENCE 433 AA; 48342 MW; 4934702460B02EE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 -- QMFINT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 NIEQSFNESPNDFSILHQECNNGLNIPINNIFIDAENNPH------ILLQQTVTPHQN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 NVISDLKKIEDLIOSMHIDA-----TLYTESDVHPSCKVTAMKCELLELOVISLES 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 SISIQCYLCLLLN-----SHELTEAGIHVF-----ILGCFSAG--LPKTEANWV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 NINEKCYMPIFSNEIVSRLSGNVSHITHKLSSTIFSSVYSTVEGAFKKGYIVDNTQCNWK 65
                                                                                                                                                                                                                                                                                                                       32;
                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                   10.7%; Score 89; DB 1:
21.9%; Pred; No. 0.46;
                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.6%; Score 96.5; DB 19.7%; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                     28; Mismatches
                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38; Mismatches
                                                                                                                                                                                                                                                                                                                                                               AD25C70C57665B3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                    500 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 AA.
                                                                                                                                                                                                                                                                                                                            DB 16; Length 167;
                                                                                                                                                                                                                                                                                                  50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16; Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66; Indels
                                                                                                                                                                                                                                                                                            36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                 68NX80
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00913; ADH_IRON_1; 1.
                   Pfam; PF00465; Fe-ADH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                          Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL; AP003186; BAB80155.1; -.
                                 InterPro; IPR001670; Fe-ADH.
                                                                                Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H., "Complete genome sequence of Clostridium perfringens, an anae.
                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=13 / TYPE A;
                                                                                                                                                                                                      Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                   PubMed=11792842;
                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                              ADH OR CPE0449
                                                                                                                                                                                                                                                                                       Alcohol dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                               ; 68NX80
                                                                                                                                                                                                                                                                                                                                                                               68NX80
                                                                                                                                                                                                                                                                                                                                                                                                                                     267 S----DCKKLPVSLIKLNCGYCYIYDFKFLEPLINLQKLNISSN 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 TESGCKECEELEEKNIK------EFLOSFVHIVOMFINTS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 NLEILDVSSNEYSNISDCKLPVSLIKLNCEFCYIYDFKFLETLNNIKIL-NISYNKNSNI 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 NECKII-DFKFLESLINLEILDVSYNKNSNIYECTLPISLIELKCISCKIIDFKFLESLI 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L., Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 ELQVISLESGDAS------IHD-----TVENLIJLANNSLSSNGNV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 NWYNVISDLKKIEDLIQSMHIDATLYTESDVHP-----SCKVTAMKCF--LL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=TUCSON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.; "The genome of Melanoplus sanguinipes entomopoxvirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99102612; PubMed=9847359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1995 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0RF MSV008 leucine rich repeat gene family protein, similar to Amsacta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=83191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Melanoplus sanguinipes entomopoxvirus (MSEPV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 IYKCKESSLEKNENCNBCKTIDFKFE-ESLINLEIEDISYNKNSNIYKCKESSLEKNENC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9YW85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 ISKPHLRSI--SIQCYLCLLLNSHFLTEAGIHVFILG-----C-FSAGLPKTEA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49;
                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       500 AA; 58567 MW; 75DC7F13BBFBCAA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.6%; Score 88.5;
21.8%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                 382 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12; Length 500;
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73; Gaps

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                                                                                                                                                                                                                                                                                          DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                               Db
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Best Local S
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Complete proteome.
SEQUENCE 382 AA; 40823 MW; 80300D0269F22E32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila virilis (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                061493;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 061493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phistry M., Sunio A., Kramer H.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF044926; AAC09301.1; -
FlyBase; FBgn0024376; Dvir\hook.
FlyBase; FBgn0024376; Dvir\hook.
SEQUENCE 678 AA; 77198 MW; 1B8535E80F06C673 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 HPSCK-VTAMKCFLLELQ----VISLESGDASIHDTVENLIILANN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 LMGADCLKDAGDQVGELG-FKKALIVTD-KVLGQIGIVKKVTDVLDNKNIEYAIYDETKP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 LLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKIEDLIQSMHIDATLYTESDV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 ----TESGCKECEELEEKNI-----KEFLOSFVHIVQM 157
                                                                                                                                                                                                                                                                                          124 VNCAKKQSYICEIMCLEEELQANIMRALQELESSTRQTTEGGVVSSLSRNSLSGMLDGNA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 10.6%; Score 88; DB 5; Length 678;
Local Similarity 23.3%; Pred. No. 3.2;
hes 37; Conservative 26; Mismatches 46; Indels 50; Gaps
                                                                                                                                                 184 KALEERDAMAOKCEETEKKMLLLIDEKTNLQQELHKLQL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                   64 NWRLRWSNLKKVVEGVYEYYSDVLNYTLOHDEVKPDVQATAEKCDLSELERLLQLVLGCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 NWVNVISDLKKIEDLIQSMHIDATLYT--ESDVHPSCKVTAMKCFLLELQVI------ 98
                                                                                                                                                                                                                                                                                                                                                                99 ------LANNSLSS--NGNV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 678 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Gaps
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